

[illegible]

FIGURE 1C

500000	TCGAGCCGACAI GGAXGACCTGAXCCCTGCTGCGAGCCIXTCGCGAGCTCCGACCGGACCTCGCCCTCGCA	764
500010C..T...A.....C...G...A.....	761
500020GCG.....GCC..T...C..A...I.....A...I.....	770
500030G.....A.....C..G.....T.....C.....G.....	
500040	GCTCGACITCGCGAAGXGCCCGGAGCGCGGACGCGGCGCTTAGCGGCCITTCCTGGAGAGCGCTCGACGTTT	
500050AA.....A.....A.....	834
500060GG..C..C..C..CACA...A...T.....T...GC...T...C..T.....	831
500070C.....C.....C.....C.....C.....	840
500080	CCGAGCGCTCGTCCAGCAGTTCCGCCCTCGTGGAGGCCCGCGAAGCGCCCTGGAGCGCGCGCGCTCGCCCGCGCG	
500090T....AA.....	904
500100G...G...GCCA.....	901
500110C...GCCG.....	910
500120	CGGAGCGCGCCCTTCGTGGGCTTTCCTTCGCGCGCGCGAGCGCGCAITGCGCGCGAGCTTCGCGCGCTCGCG	
500130G.....AAG.....T.....	974
500140TC..T.....T.....	971
500150C.....C.....AAA.....	980
500160	CGCGCGCGAGGAGCGCGCGCTCCACCGGGCGGACGAGACCGCTTTAXGCGCGCTXAGCGGACCTXAAGCGAGTGC	
500170C...G...T.A..AA..C...C.....G.....	1044
500180G.....T.....A.....G.....T.....G.....	1041
500190G..CC...T.....C.....GCC...G..A.A.....C.....	1050
500200C.....G.....C.....	

Sequence	Position
CGGGGXCCTCGTCCCAAGCAGCTGGCCGTCTGGCCCTGAGCGAGCGCTXGACCTCXTCGGCGGGGAGG	1114
.....	1111
.....	1120
.....	1184
.....	1181
.....	1190
.....	1254
.....	1251
.....	1260
.....	1324
.....	1321
.....	1330
.....	1394
.....	1391
.....	1400

Position	Sequence	Position	Sequence
1464	GGAGATCCCGCGCGCTCCAGGAGGAGGCTCTCCGCGCTGGCGCGCGCGCGCGCTCAACCTCAAGTCCCGCGGAG	1674	CCGGCAGCTCACCAGCTCAGAGACACCTAGATXGACCGCGCTCCGCGCGCGCTCCGCGCGCGCGCGCGCGCGCGCG
1465	CC	1675	CC
1466	GCAGG	1676	CC
1467	GCAGG	1677	CC
1468	GCAGG	1678	CC
1469	GCAGG	1679	CC
1470	GCAGG	1680	CC
1471	GCAGG	1681	CC
1472	GCAGG	1682	CC
1473	GCAGG	1683	CC
1474	GCAGG	1684	CC
1475	GCAGG	1685	CC
1476	GCAGG	1686	CC
1477	GCAGG	1687	CC
1478	GCAGG	1688	CC
1479	GCAGG	1689	CC
1480	GCAGG	1690	CC
1481	GCAGG	1691	CC
1482	GCAGG	1692	CC
1483	GCAGG	1693	CC
1484	GCAGG	1694	CC
1485	GCAGG	1695	CC
1486	GCAGG	1696	CC
1487	GCAGG	1697	CC
1488	GCAGG	1698	CC
1489	GCAGG	1699	CC
1490	GCAGG	1700	CC
1491	GCAGG	1701	CC
1492	GCAGG	1702	CC
1493	GCAGG	1703	CC
1494	GCAGG	1704	CC
1495	GCAGG	1705	CC
1496	GCAGG	1706	CC
1497	GCAGG	1707	CC
1498	GCAGG	1708	CC
1499	GCAGG	1709	CC
1500	GCAGG	1710	CC
1501	GCAGG	1711	CC
1502	GCAGG	1712	CC
1503	GCAGG	1713	CC
1504	GCAGG	1714	CC
1505	GCAGG	1715	CC
1506	GCAGG	1716	CC
1507	GCAGG	1717	CC
1508	GCAGG	1718	CC
1509	GCAGG	1719	CC
1510	GCAGG	1720	CC
1511	GCAGG	1721	CC
1512	GCAGG	1722	CC
1513	GCAGG	1723	CC
1514	GCAGG	1724	CC
1515	GCAGG	1725	CC
1516	GCAGG	1726	CC
1517	GCAGG	1727	CC
1518	GCAGG	1728	CC
1519	GCAGG	1729	CC
1520	GCAGG	1730	CC
1521	GCAGG	1731	CC
1522	GCAGG	1732	CC
1523	GCAGG	1733	CC
1524	GCAGG	1734	CC
1525	GCAGG	1735	CC
1526	GCAGG	1736	CC
1527	GCAGG	1737	CC
1528	GCAGG	1738	CC
1529	GCAGG	1739	CC
1530	GCAGG	1740	CC
1531	GCAGG	1741	CC
1532	GCAGG	1742	CC
1533	GCAGG	1743	CC
1534	GCAGG	1744	CC
1535	GCAGG	1745	CC
1536	GCAGG	1746	CC
1537	GCAGG	1747	CC
1538	GCAGG	1748	CC
1539	GCAGG	1749	CC
1540	GCAGG	1750	CC
1541	GCAGG	1751	CC
1542	GCAGG	1752	CC
1543	GCAGG	1753	CC
1544	GCAGG	1754	CC
1545	GCAGG	1755	CC
1546	GCAGG	1756	CC
1547	GCAGG	1757	CC
1548	GCAGG	1758	CC
1549	GCAGG	1759	CC
1550	GCAGG	1760	CC
1551	GCAGG	1761	CC
1552	GCAGG	1762	CC
1553	GCAGG	1763	CC
1554	GCAGG	1764	CC
1555	GCAGG	1765	CC
1556			

FIGURE 1F

1814	AGAACAI	CCCCCGT	CCCGACCC	CCXCT	CGGGCC	AGAGGAT	CCCGCC	GGCCCT	TGGT	GGCC	AGCG	CGGCT	GGG	1814
1811														1811
1820														1820
1884	GTTCG	TGGCC	CTGGAC	TATAC	CCAGAT	AGGCT	CGGG	CTCC	TGGCC	AGGCT	CTCC	GGG	AGG	1884
1881														1881
1890														1890
1954	ATCCG	CGTCT	CCAGG	GGG	AGG	ACAT	CCAC	ACG	AGCC	CCAGG	CTGG	ATG	TCCG	1954
1951														1951
1960														1960
2024	AGCCG	GTG	ACCC	CGT	CA	TGCG	CGCG	GGG	CGA	AGCC	ATCA	AGCT	TCGG	2024
2021														2021
2030														2030
2094	CCAC	CCCC	CTCT	CCAG	AGG	CTT	CCCA	TCCC	CTAC	CGAG	GGG	GTCC	CTT	2094
2091														2091
2100														2100

[illegible]

FIGURE 1H

5'-GAGT	CCCCCTGGAGGTGGGGATCGGGAGGACTGGCTCTCGGGCAGGACTAG	2498
3'-CTATA.....GA	2496
5'-GATCC.....GT...	2505

FIGURE 2A

SEQUENCE	MRAMLPLEPKGAVLLVDGHHLAYRIFFALKOLISRGEPVQAVYGFASKLKAIKEDG·OAVXVYFDAX	
100-150H.....I.....	69
150-200V.....	68
200-250YK.....F.....	70
SEQUENCE	APSPRHEAYEAYKAGRPTPEDFPROLALIKELVOLLCXRLEVPQYEADOVLATLAKNAEKEGYEVRI L	
250-300A.....S.....	139
300-350V.....F.....R.....	138
350-400F.....	140
SEQUENCE	TADRDLYOLLISORIAVLHPEGVLITPAWLWEKYGLRPEQWUDYRALXGDPSDHLPQVXGICEKTXKLLX	
400-450H.....D.....T.....E.....R.....E	209
450-500Y.....A.....I.....GR.....IR	208
500-550F.....V.....L.....K	210
SEQUENCE	EWGSLERLLKHLDRVKP·XXREKIXAHMEDLXLSXXLSXVRIOLPLEVGFAXRREPDRGCLRAFLEALEF	
550-600A.....L.....AI.....L.....D.....K.....WD,AK.....K.....R.....	278
600-650FOH.....O.....SL.....LO.....G.....A.....A.....RK.....O.....H.....GR.....T.....IL.....	277
650-700ENV.....K.....L.....R.....LE.....R.....L.....OG.....	280
SEQUENCE	GSLLHEFGLLFXPKALEEAPWPPPEGAFVGFVLSRPEPHVAELLALAAARXGRVHRAXDPLXGLROLKEV	
700-750S.....K.....D.....G.....PE.....YXA.....A	348
750-800G.....A.....L.....SF.....G.....WE.....L.....Q.....R.....G.....	347
800-850A.....AP.....K.....C.....D.....A.....A.....K.....	350

FIGURE 2B

[illegible]

FIGURE 2C

SEQUENCE	SFPKVRWIEKTLSEGRARQYVETLFGARRYPOLNARVKSVREAAERMAFHHPVOGIAADLHKLAHVKL	
768E.....	768
769	Y.....O.....	769
770K.....	770
SEQUENCE	FPRLXEHGAAAMLLOVHDEIVLEAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVOXGEDWLSAKEX	
833E.....A.....R.....	833
834O.....L.....D.....R.....W.....O.....L.....	834
835R.....L.....OA.....E.....A.....KA.....H.....G.....	835

FIGURE 3

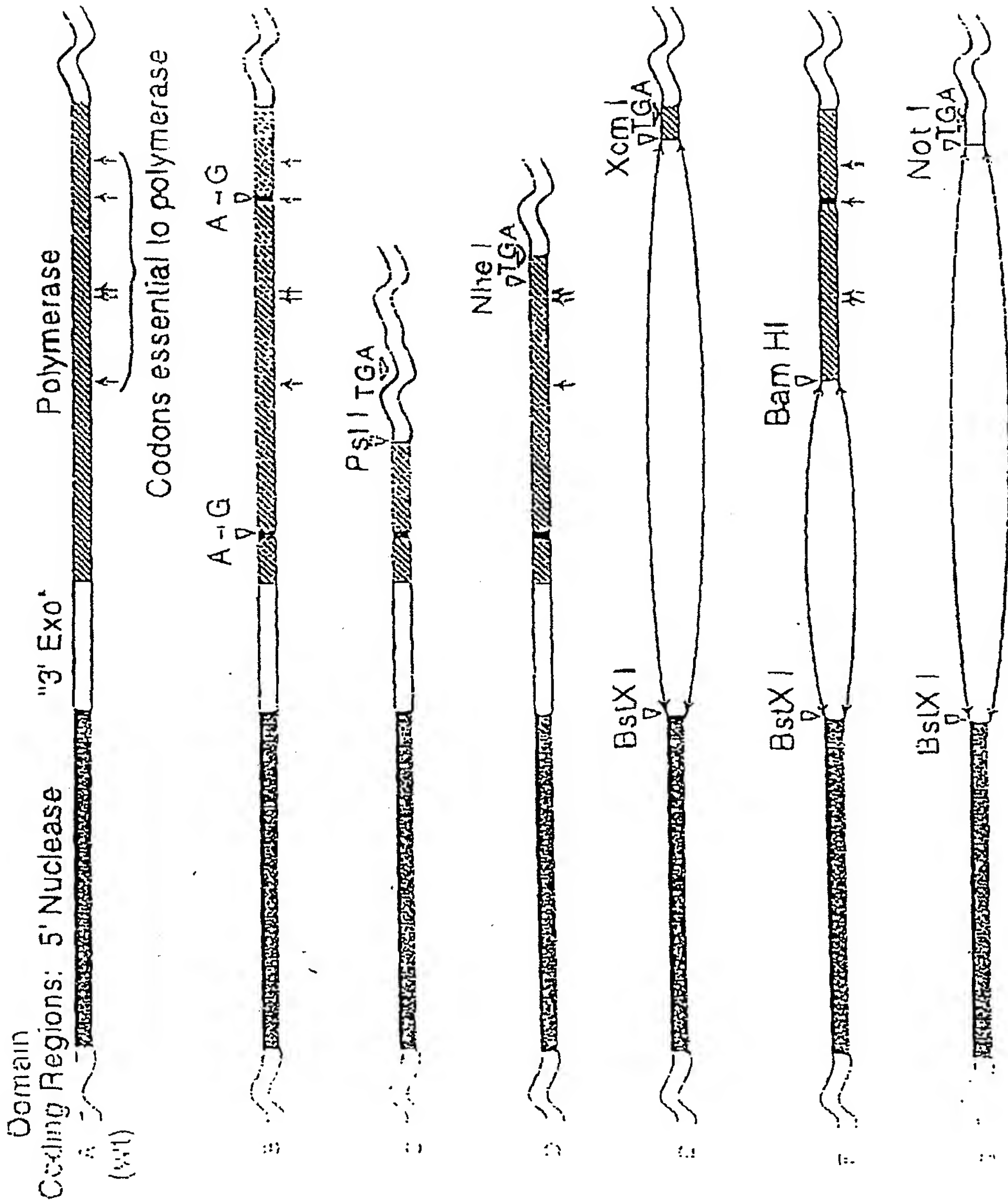


FIGURE 4

Genes for Wild-Type and Pol(-) DNAPT^H

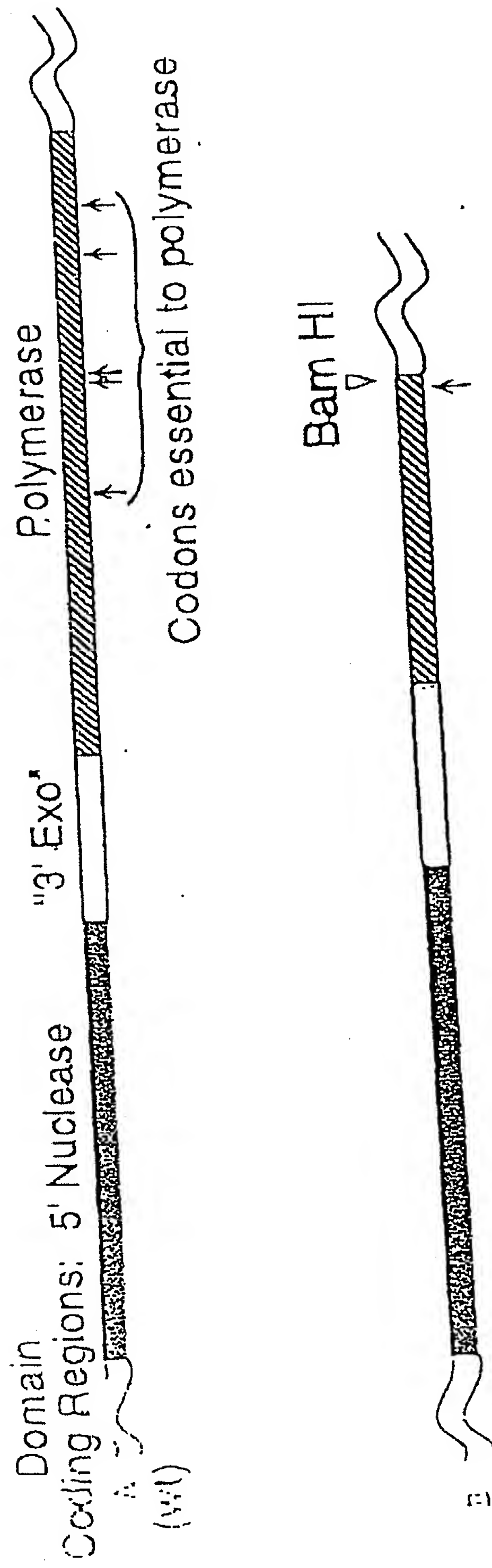
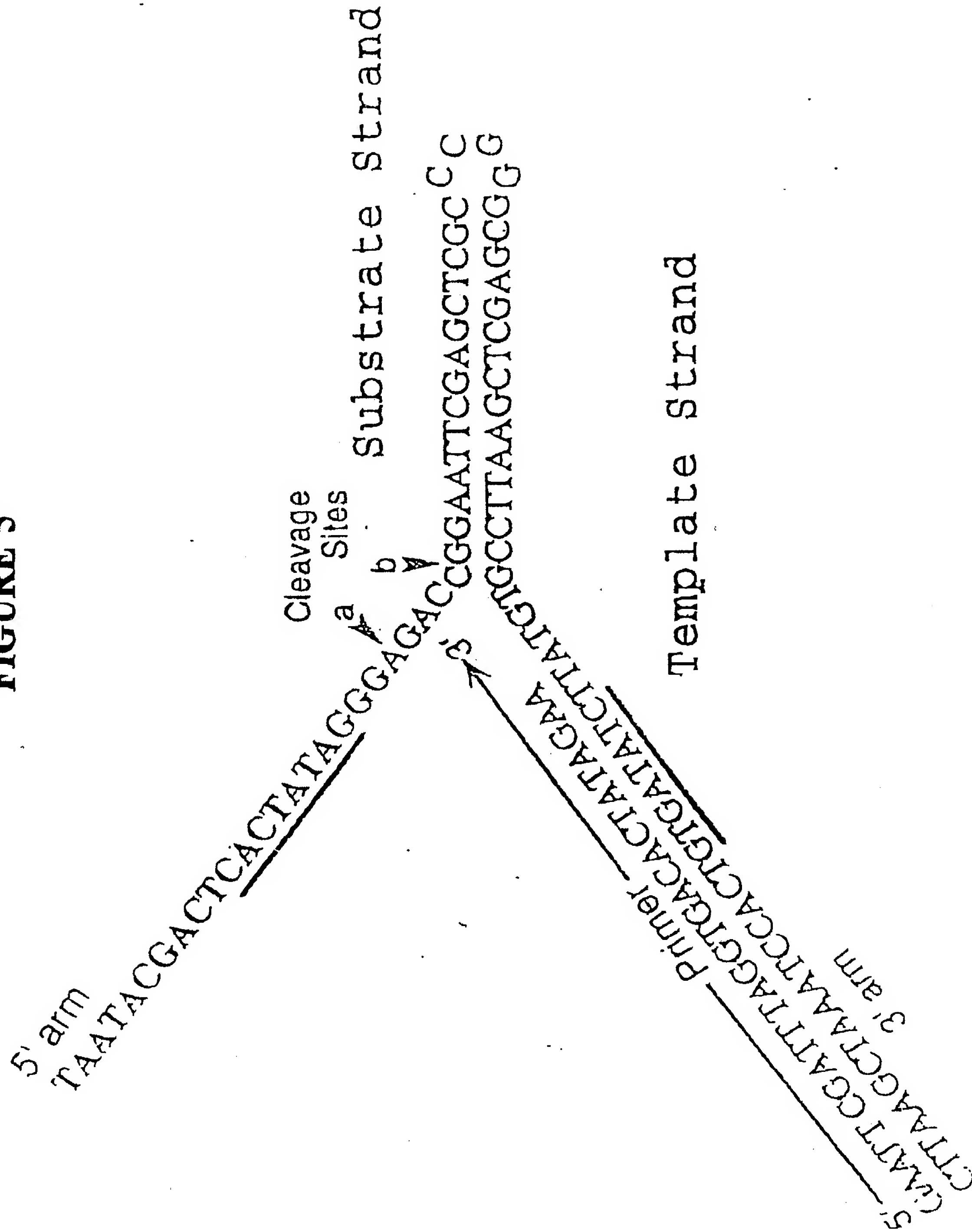


FIGURE 5



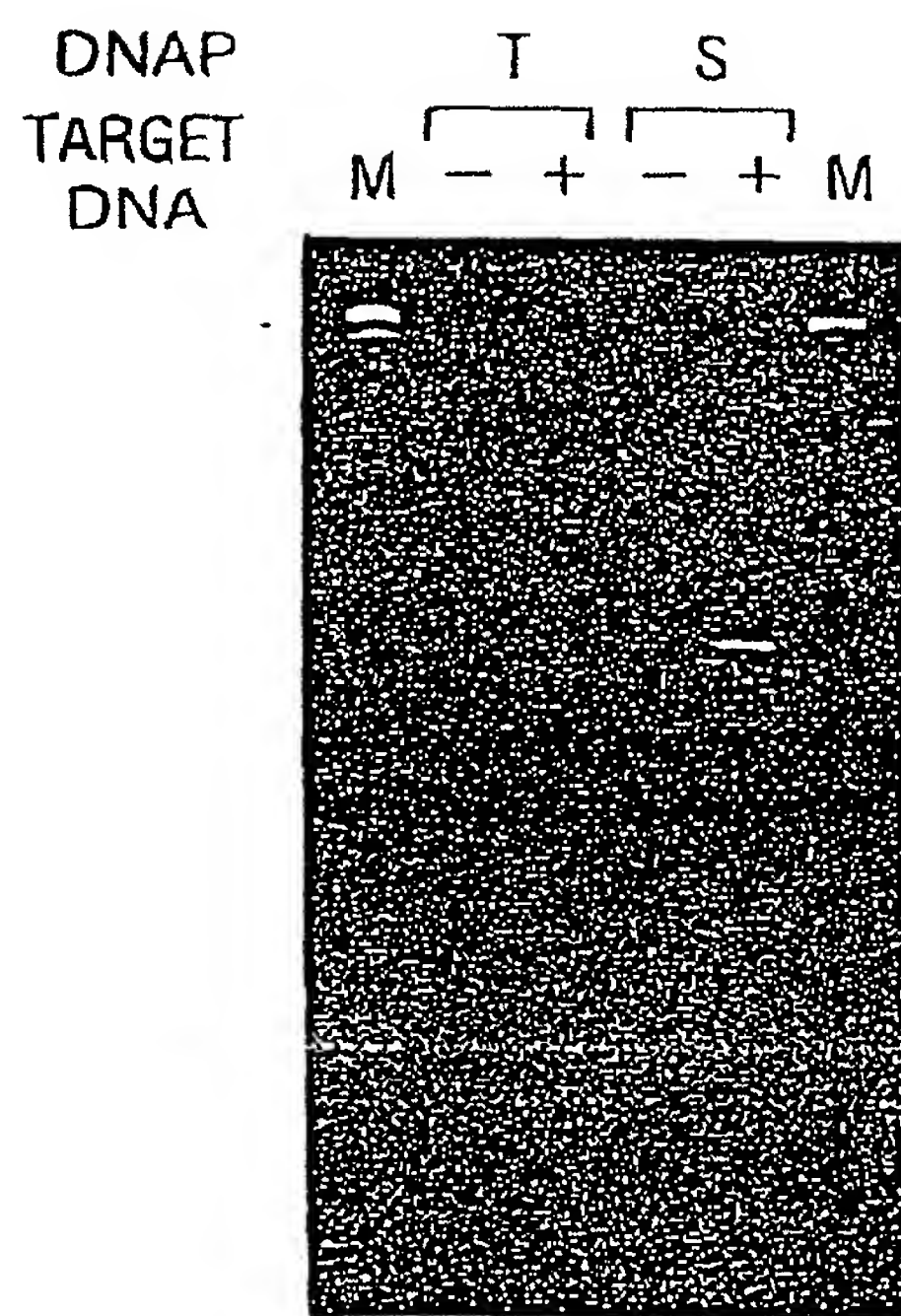


FIGURE 6

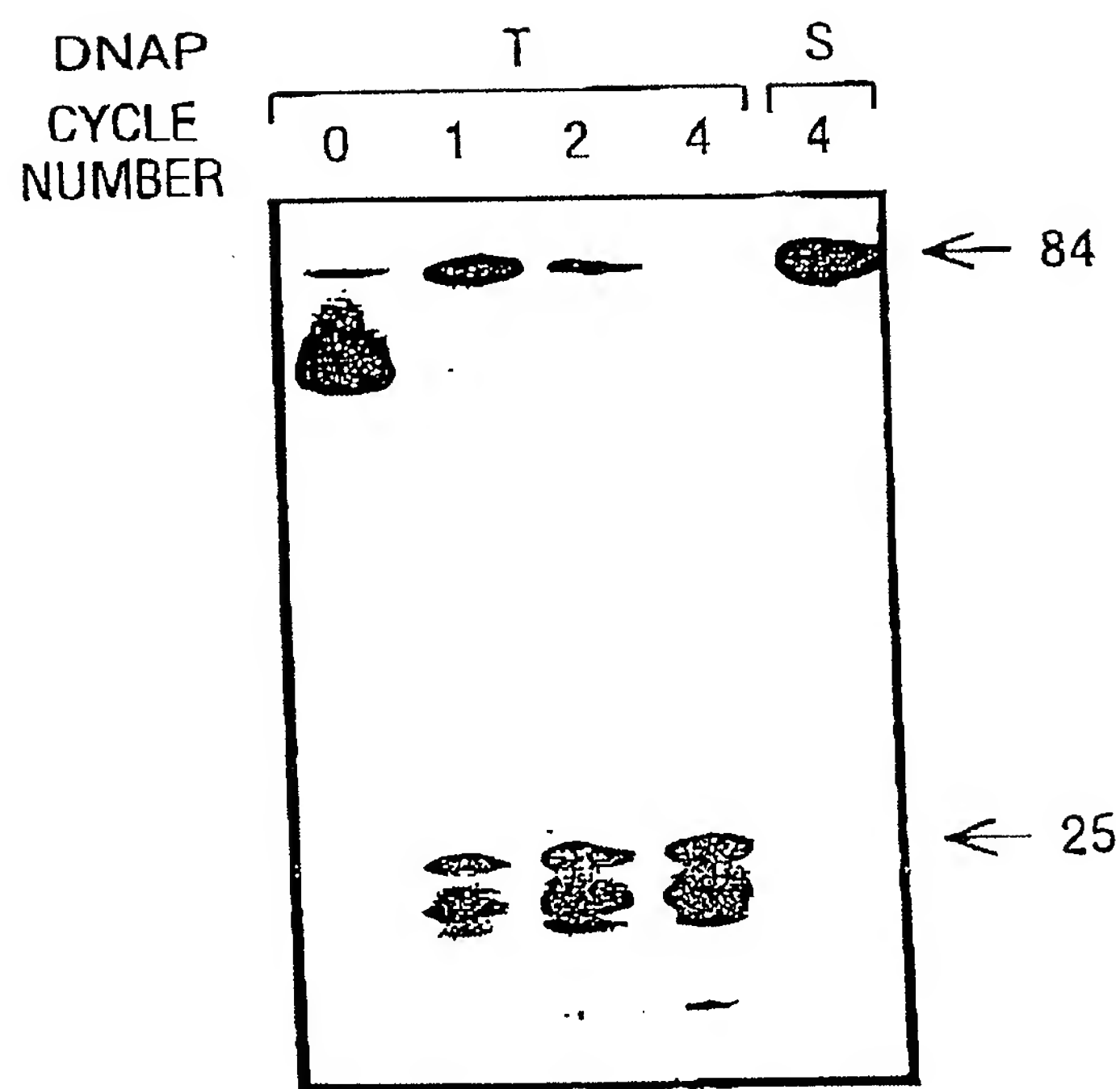


FIGURE 7

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl ₂ :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

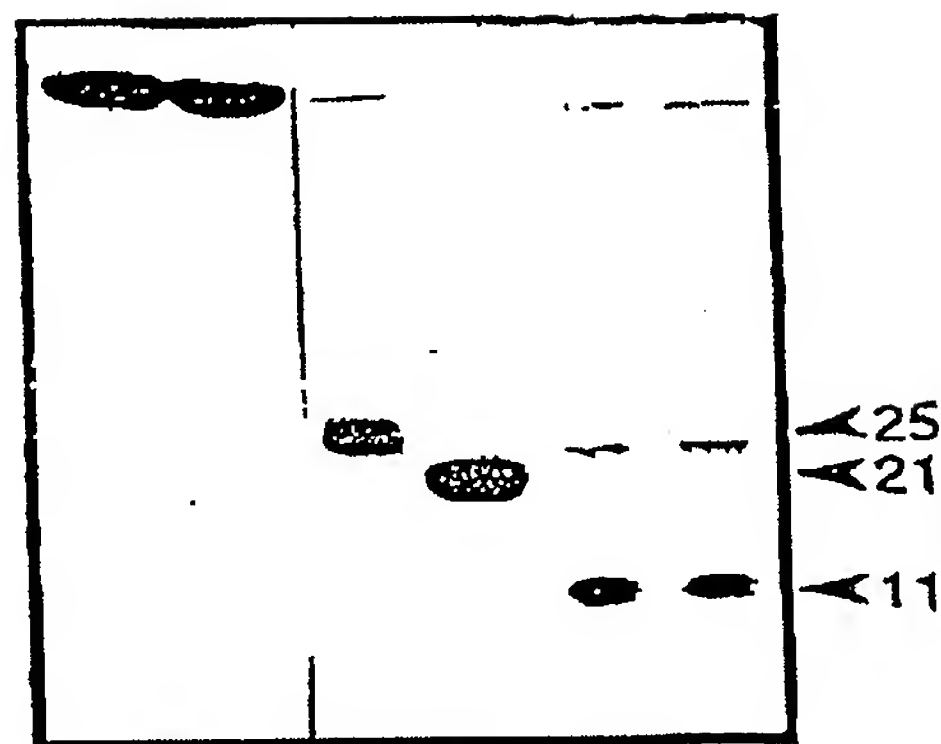


FIGURE 8A

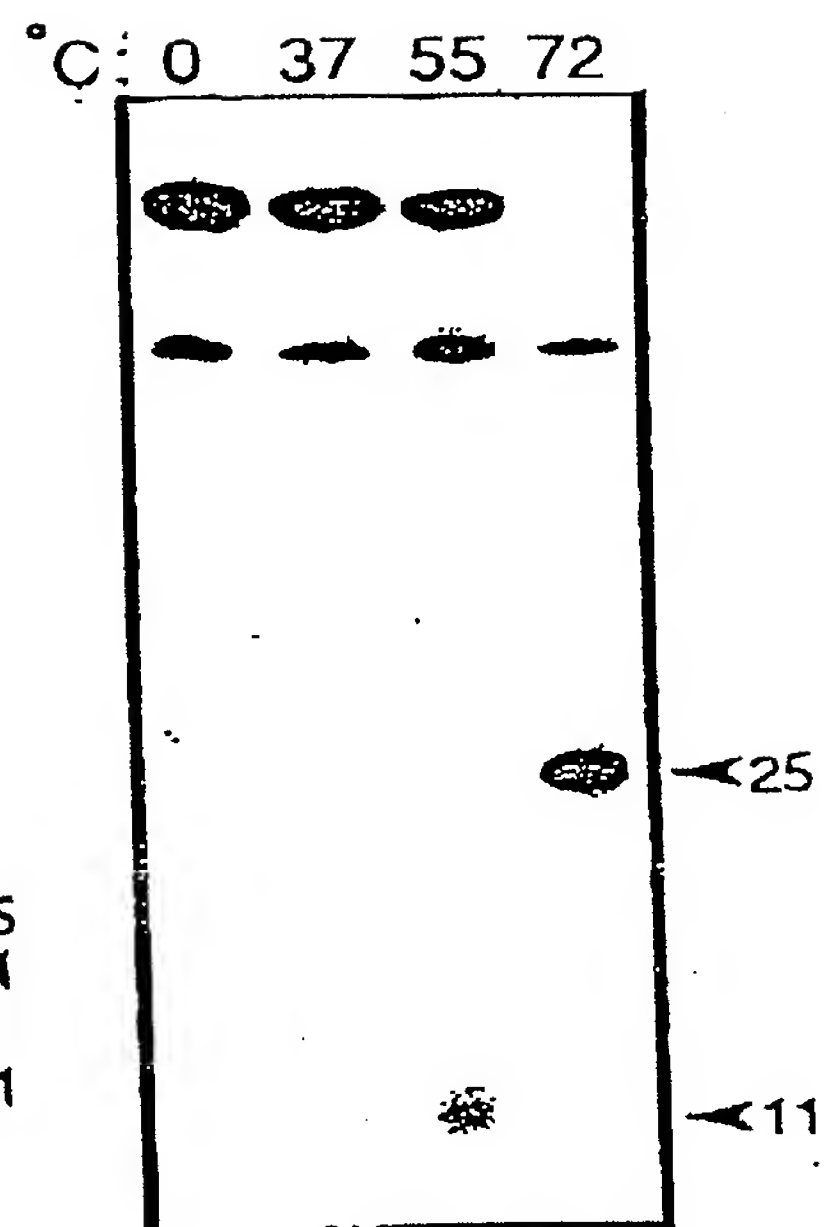


FIGURE 8B

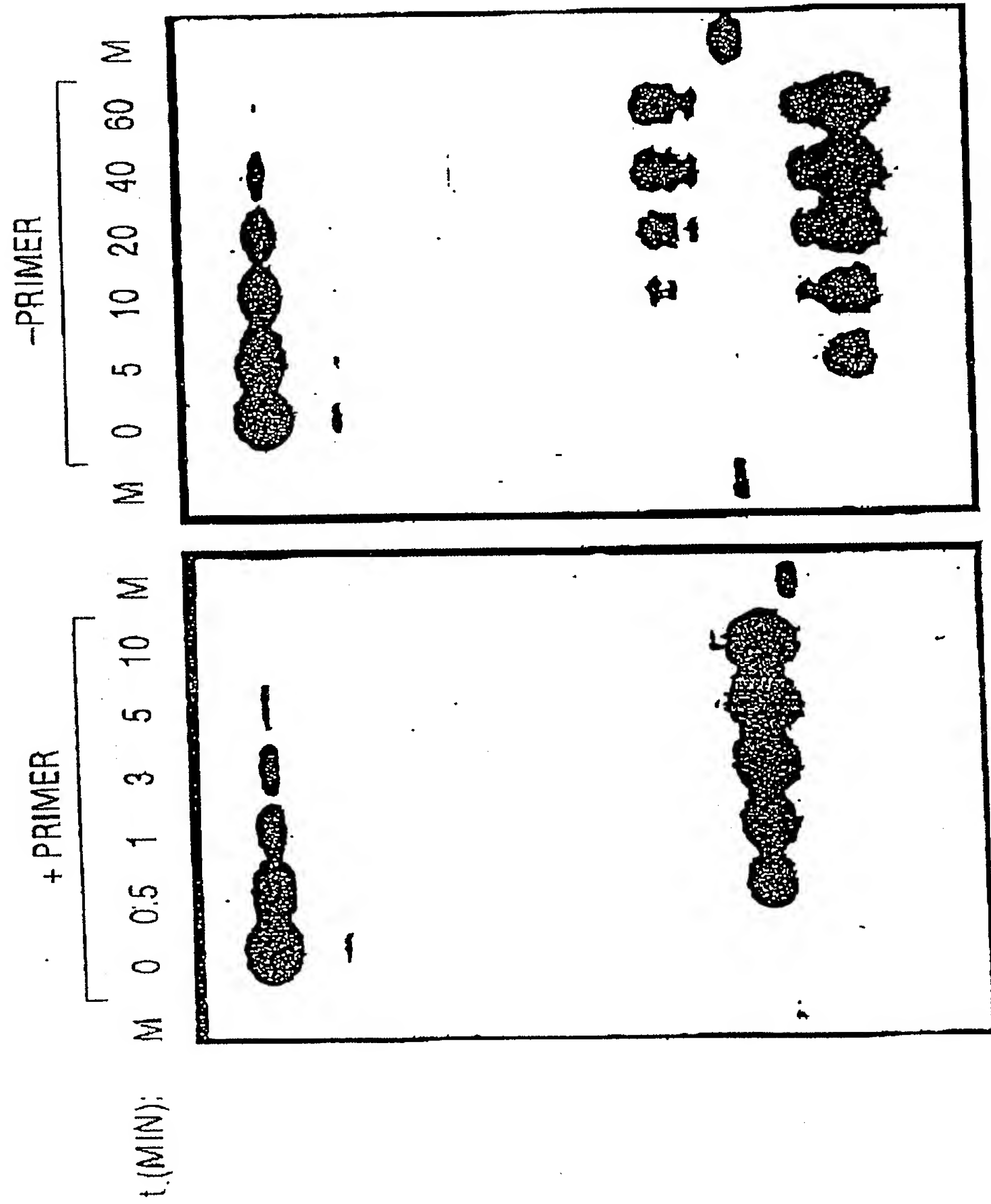


FIGURE 9B

FIGURE 9A

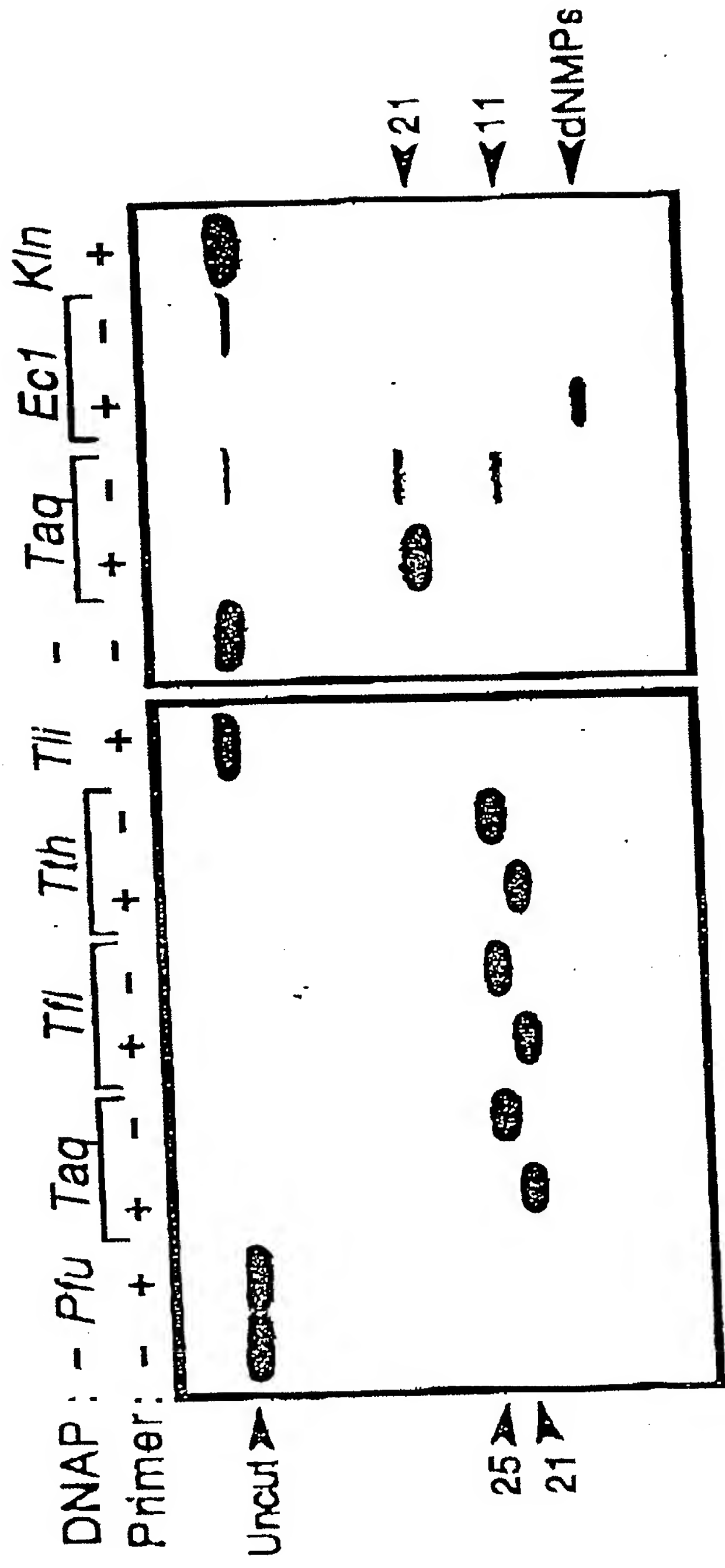


FIGURE 10B

FIGURE 10A

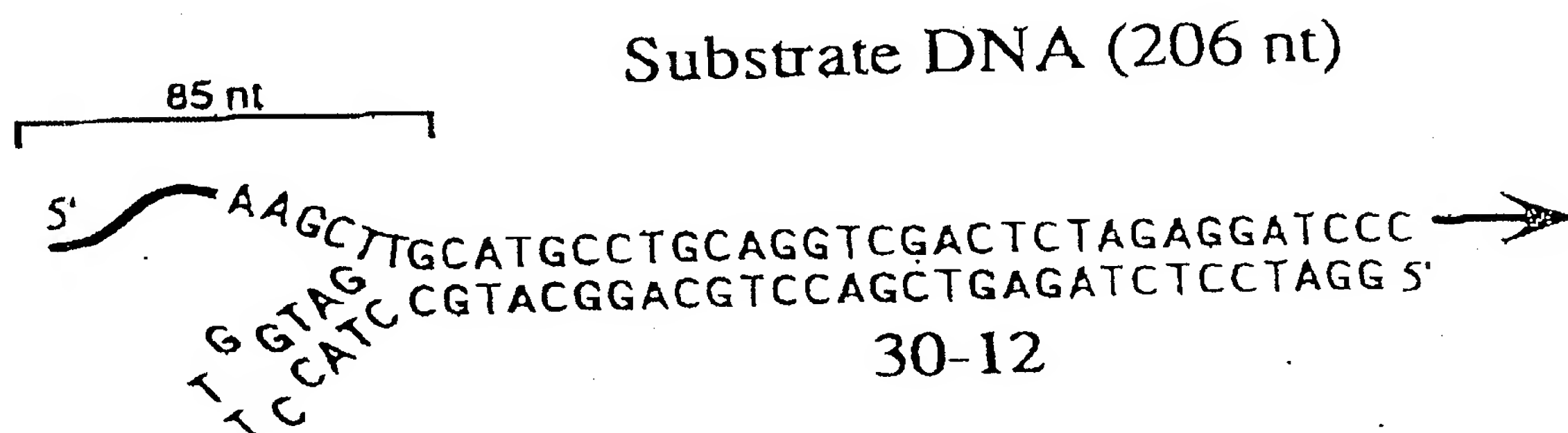
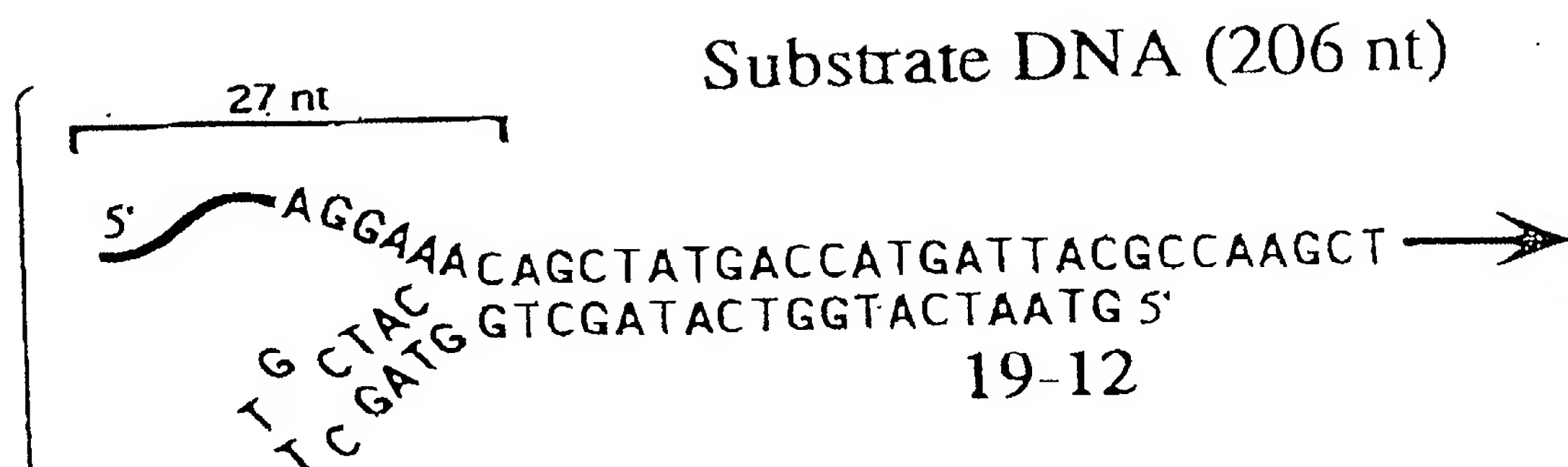


FIGURE 11A

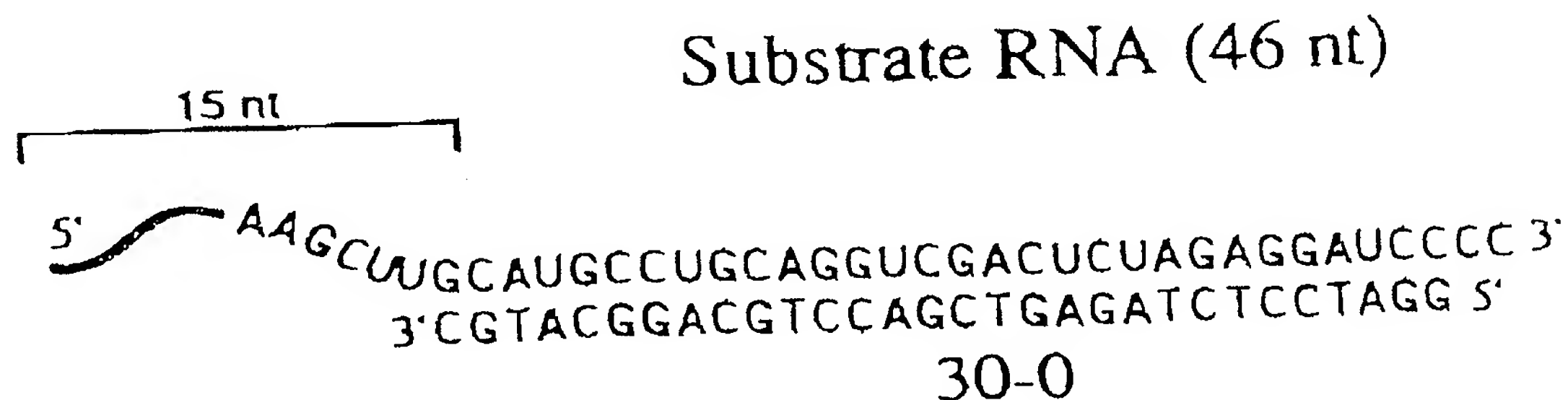


FIGURE 12A

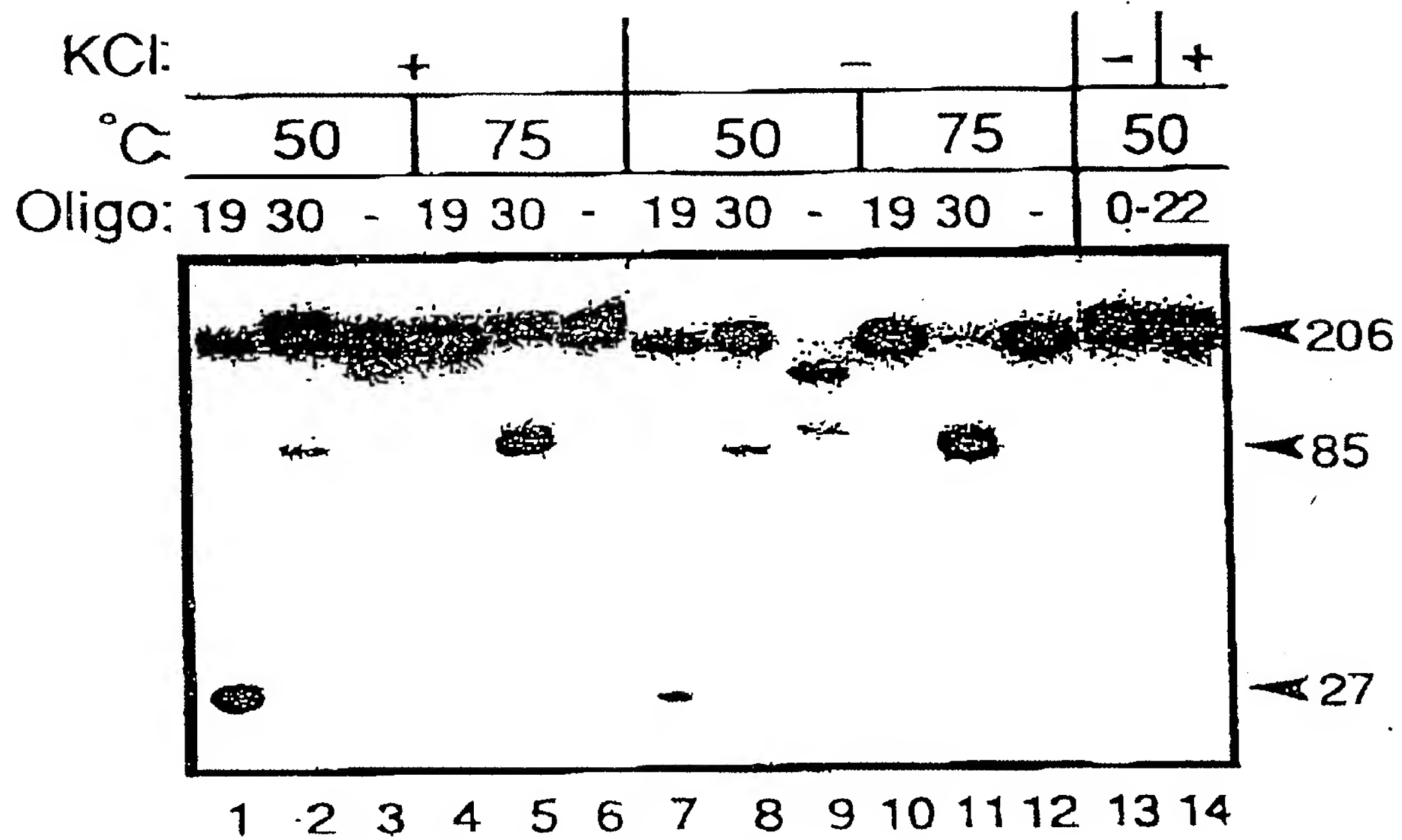


FIGURE 11B

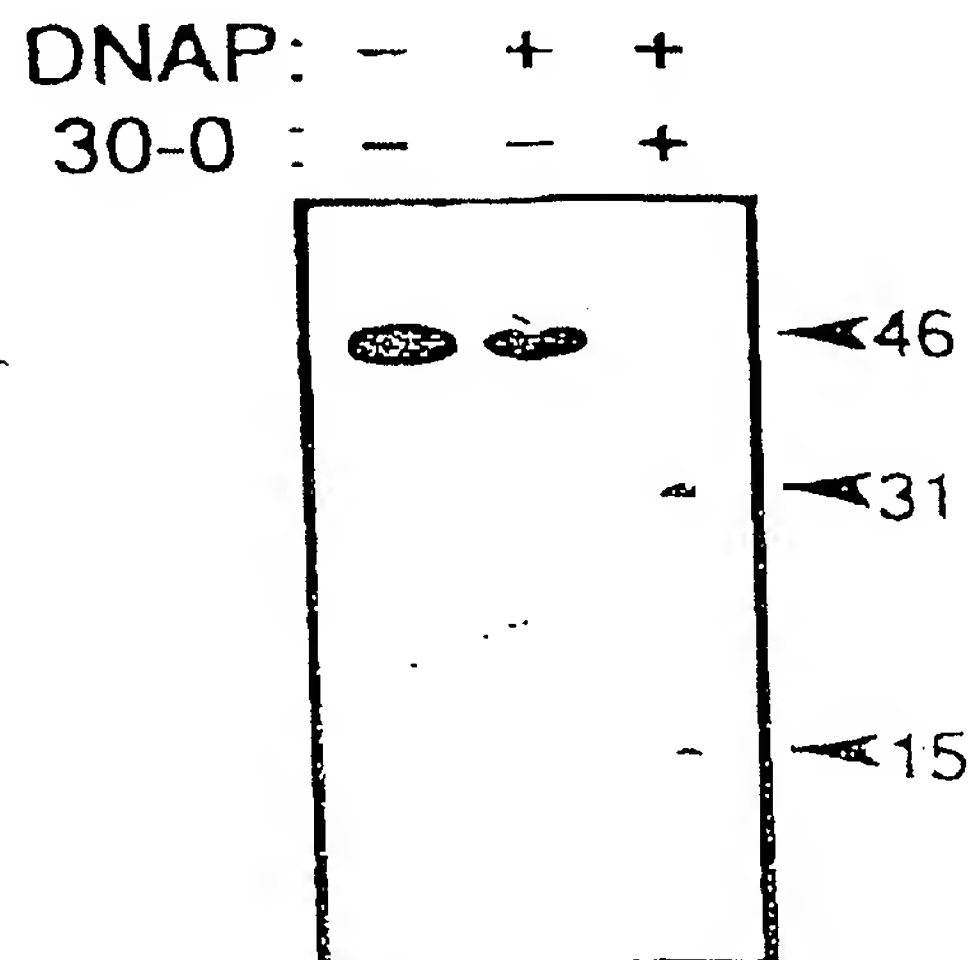


FIGURE 12B

FIGURE 13

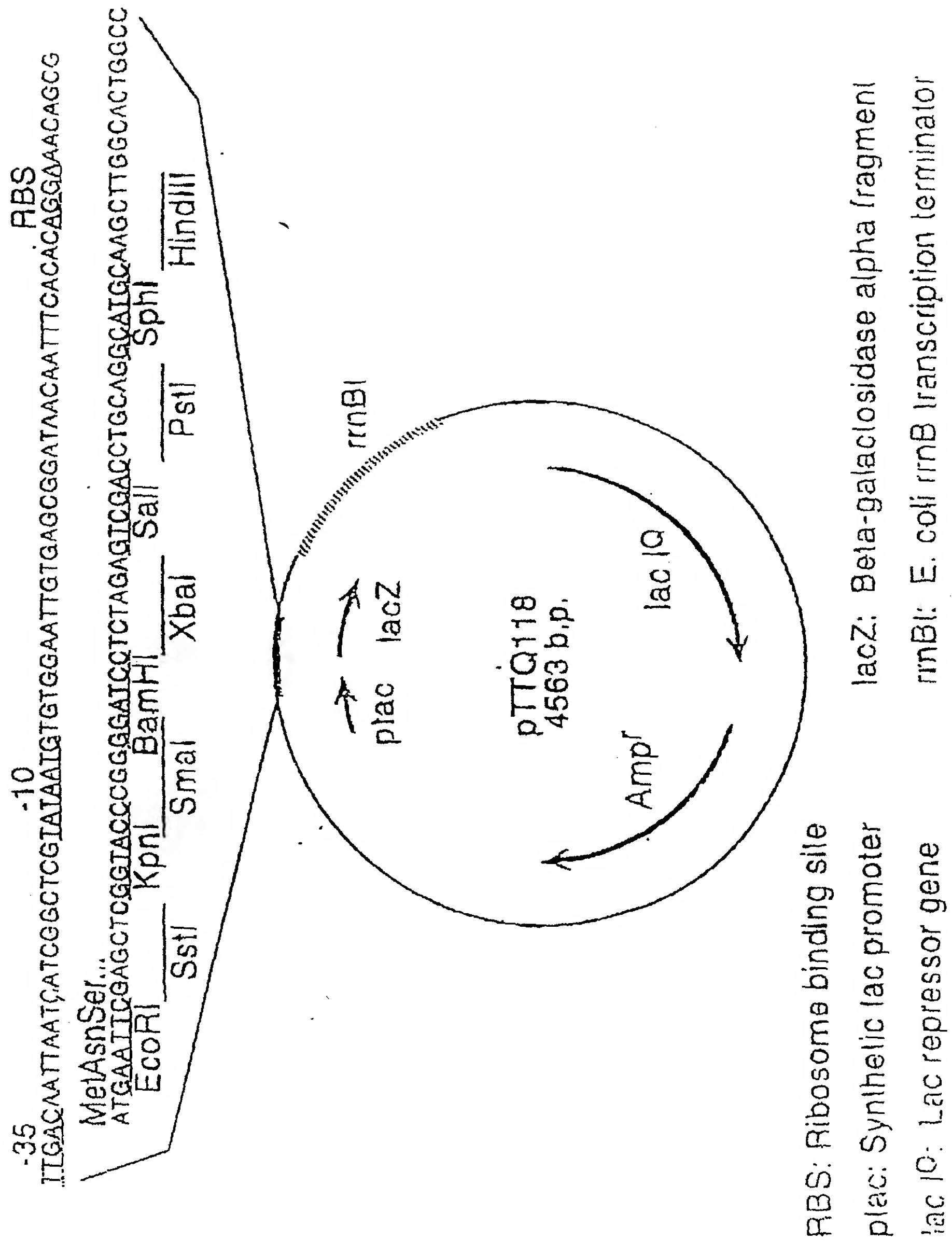
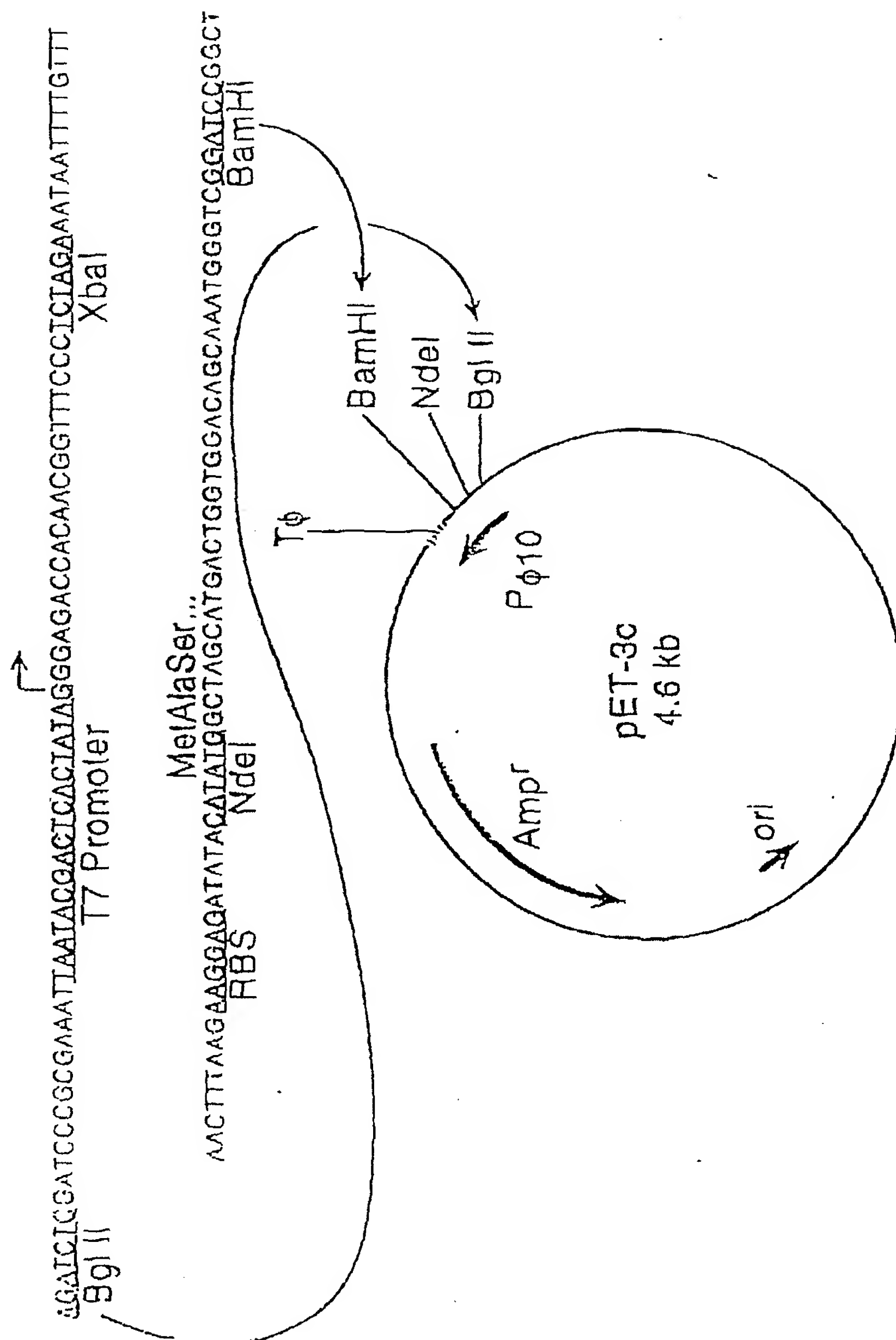


FIGURE 14



P_{φ10}: Bacteriophage T7 φ10 promoter

T_φ: T7 φ Terminator

RBS: Ribosome binding site



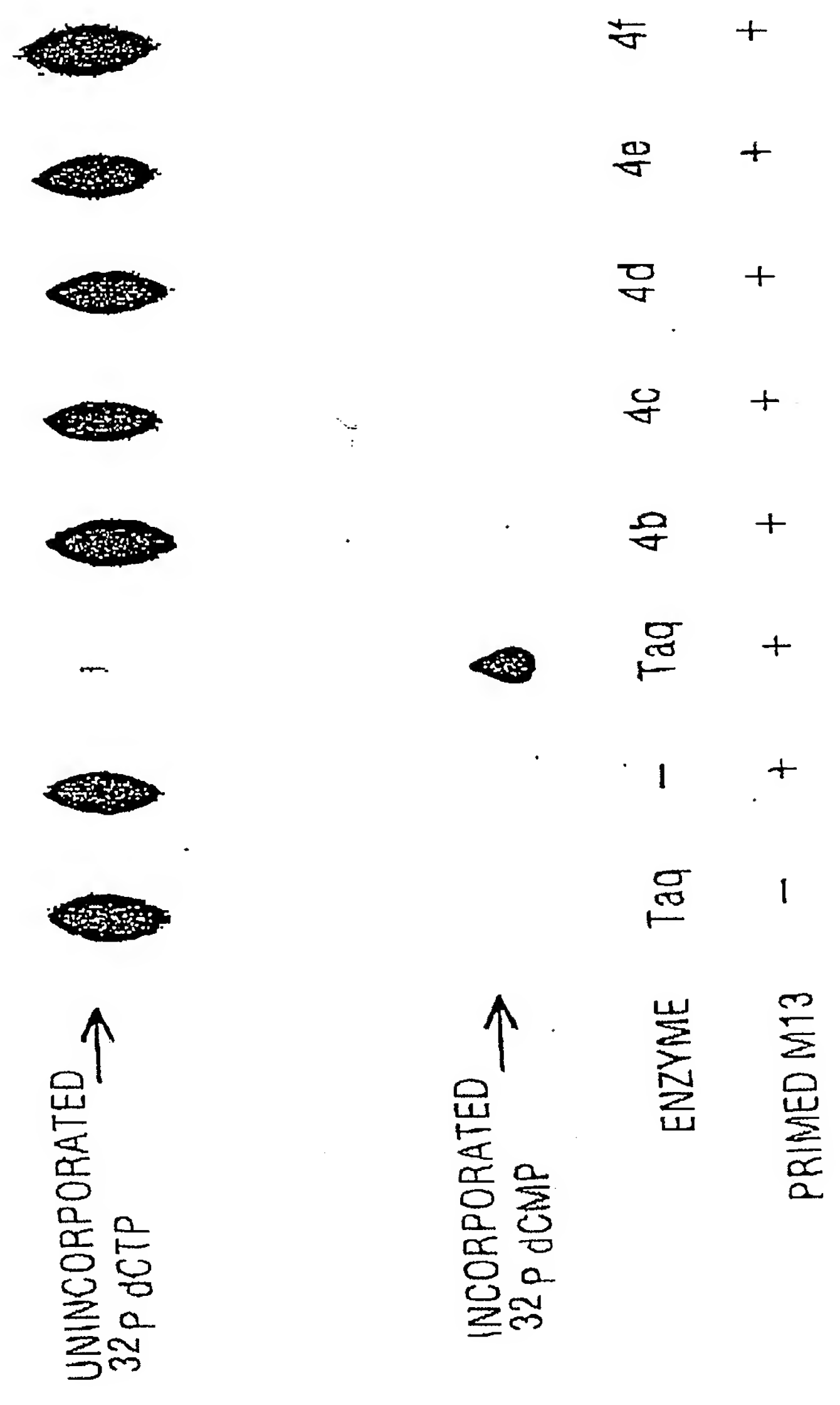


FIGURE 17

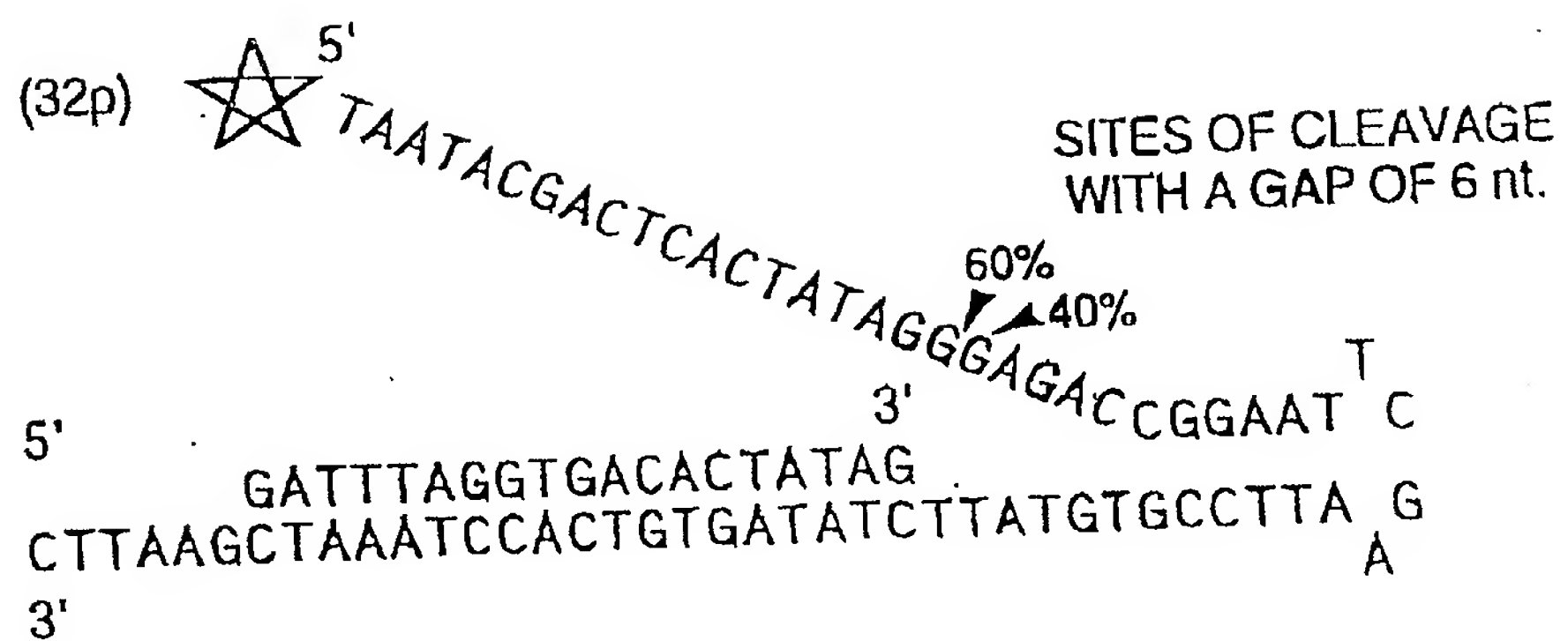


FIGURE 18A

	"4d"		"4b"		UNMODIFIED	
	NO POL. ACTIVITY		2 PT. MUTATION SMALL ACTIVITY		DNAP Taq	
1						
2						
3	-	+	-	+	7	8
4	-	+	-	+		
5						
6						
7						
8						
	-	+	-	+	-	+
						dNTP

84 NUC. ———

← HAIRPIN TEST MODULE

← CONVERSION TO DOUBLE STRANDED (COMPLETE EXTENSION OF PRIMER)

DESIRED PRODUCT 21 NUC. →

MULTIPLE BANDS CAUSED BY POLYMERIZATION

↑ SOME ABERRANT CLEAVAGE WITH "4b" BECAUSE OF RESIDUAL POLYMERASE ACTIVITY.

FIGURE 18B

Ban II
Sst I
Asp 718
Ava I
Kpn I
Xma I
Sma I
Bam HI
Xba I
EcoR I

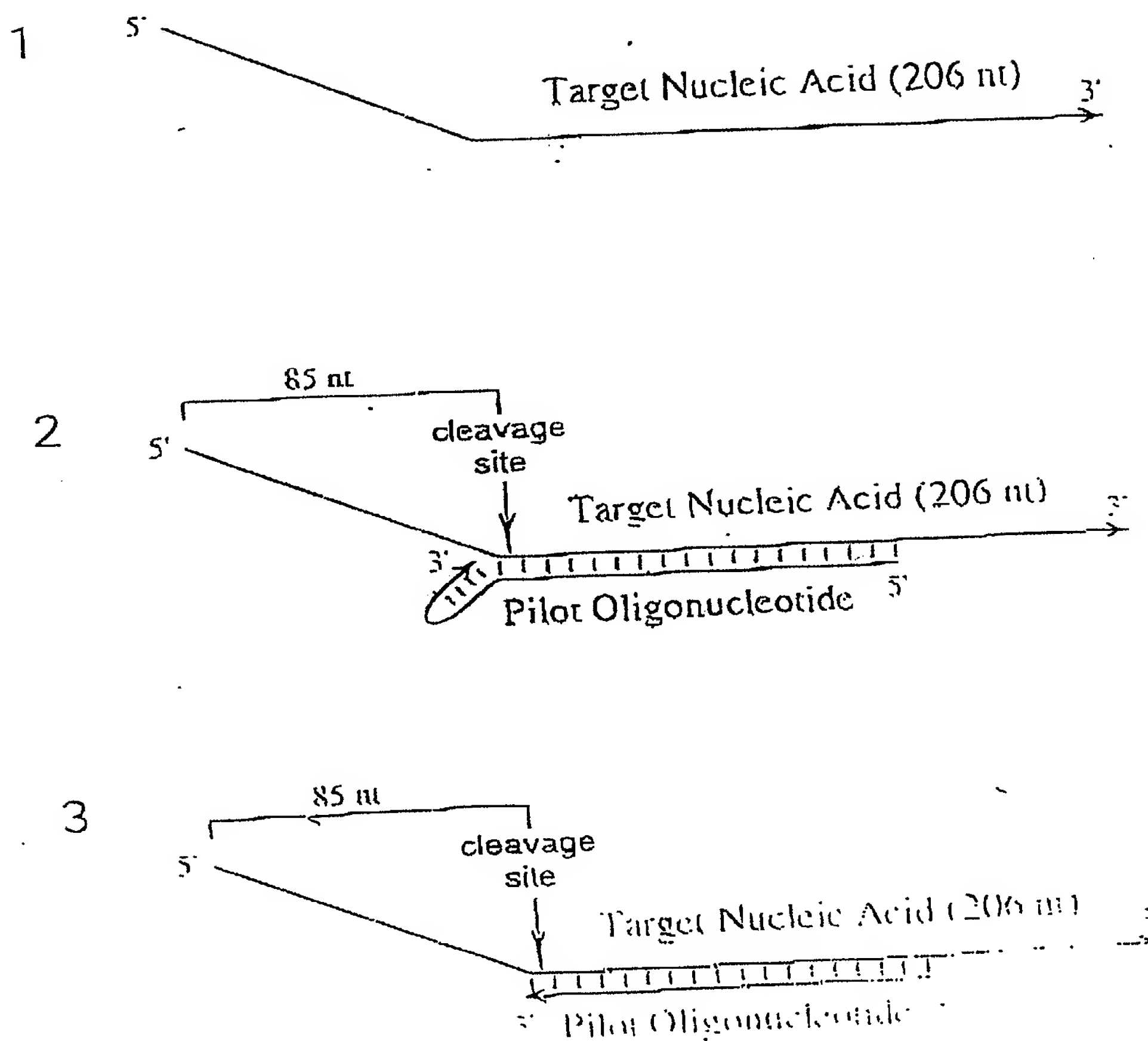
5'-TCTGCTCAGCAGCGTTGTAAACGACGCCACCTGAAATGTAAATAGCAGTCACTATATAGGCGGAATTCGAGCTCGGTACCCGGGGAATCCTC
 3'-ACACGCTGCAACATTTTCTGCGCGCTCACTTAAACATTATCTGTAGTGATATCCCGCTTAAGCTCGAGCCATGCGGCCCTTAGGAG
 (Pillai 30-0-
 T7
 5' Forward

Psu
 SspM
 Sph
 Hird III

[illegible]

228

FIGURE 20A



	I	II	III	IV	V	I	VI
	1	1 2 3	1 1 2 3	1 2 3 1	1 2 3 1	1 2 3 1	1 2 3
1	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3

— 206

— 85

206 —

85 —

FIGURE 20B

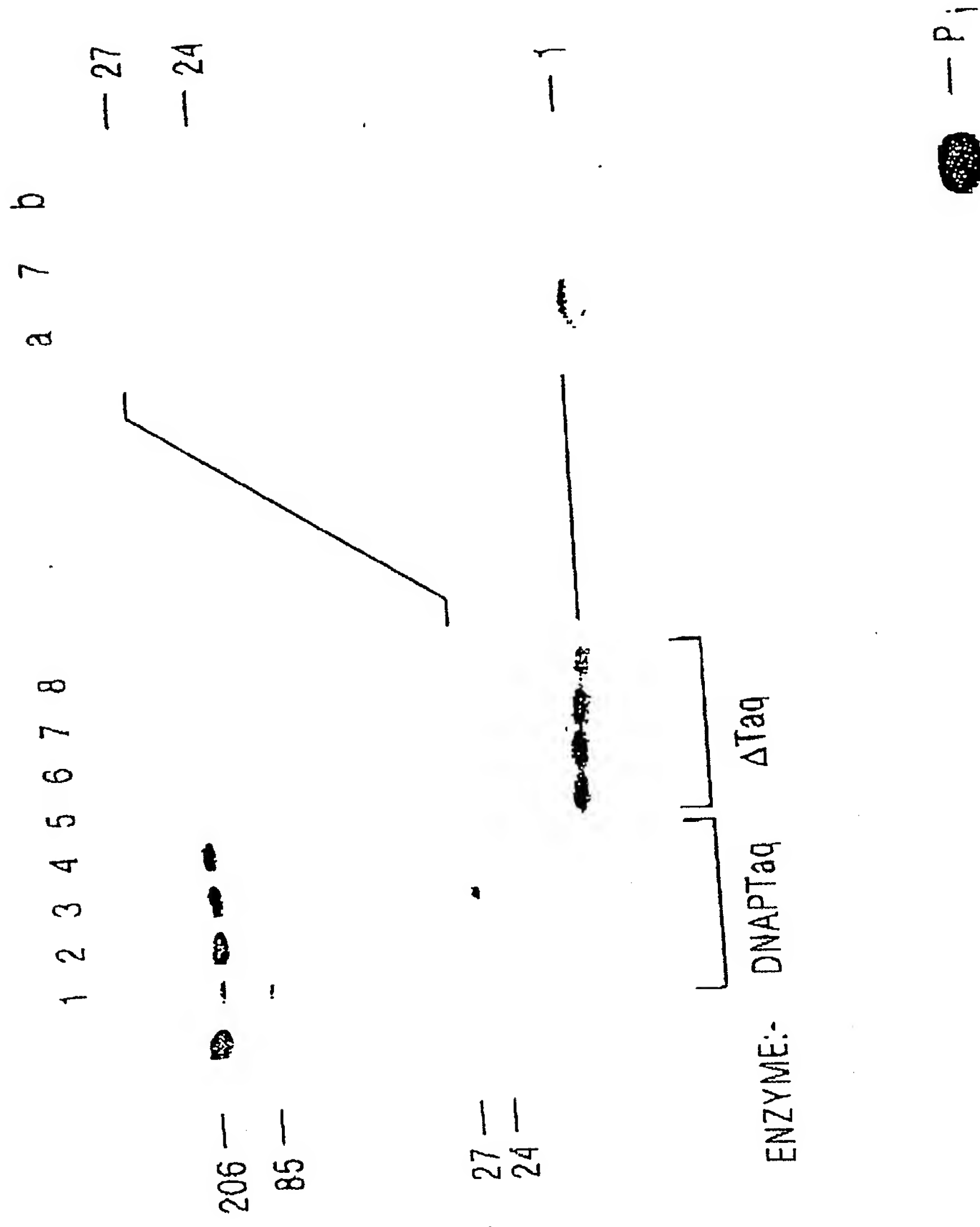


FIGURE 21B

FIGURE 21A

FIGURE 22A



— 206

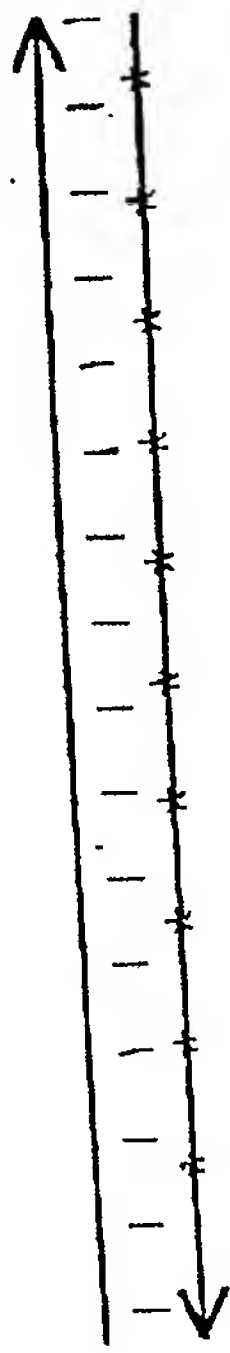
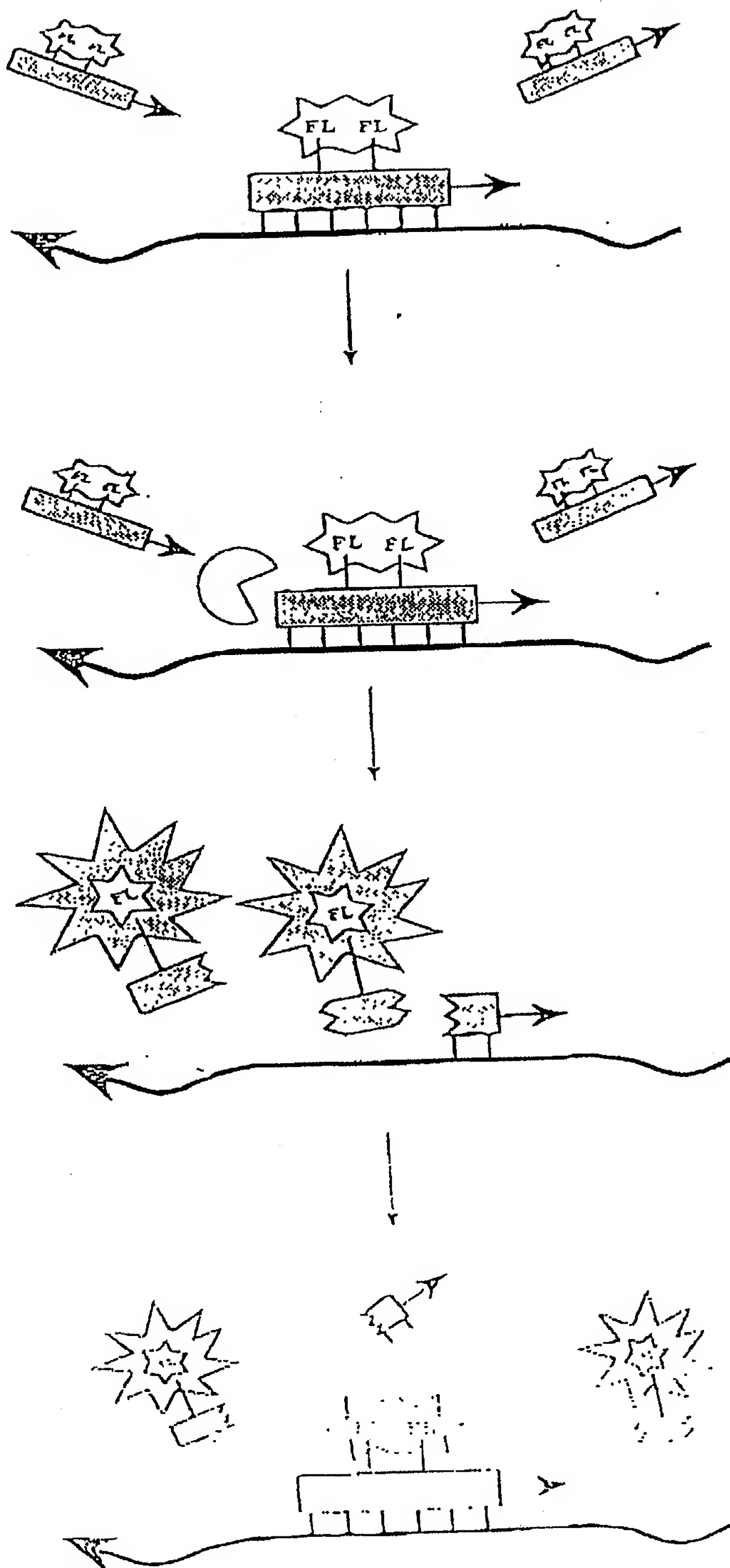


FIGURE 22B

* = 32p

FIGURE 23



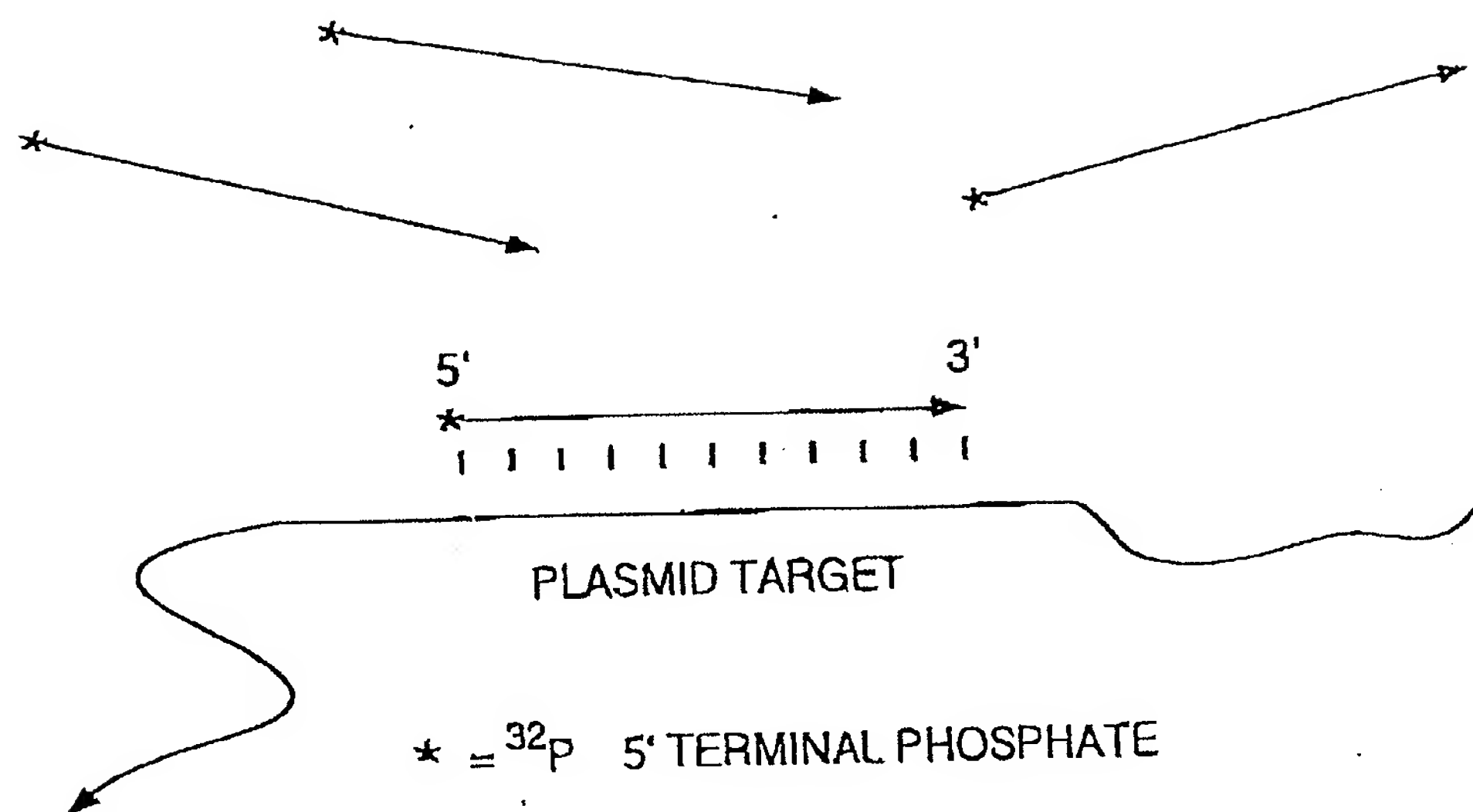


FIGURE 24A

M 1 2 3 4 5 6



FIGURE 24B

FIGURE 25

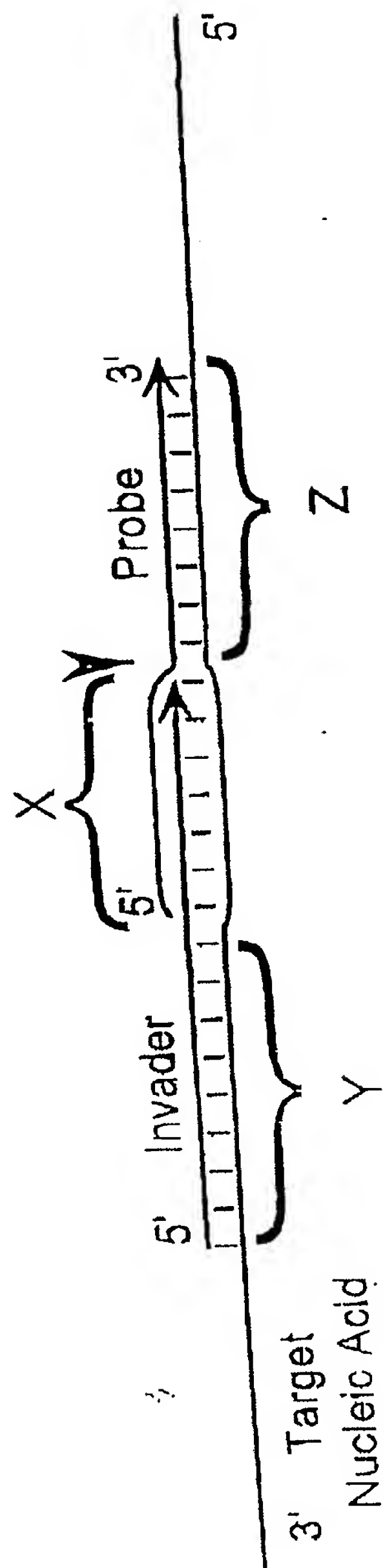
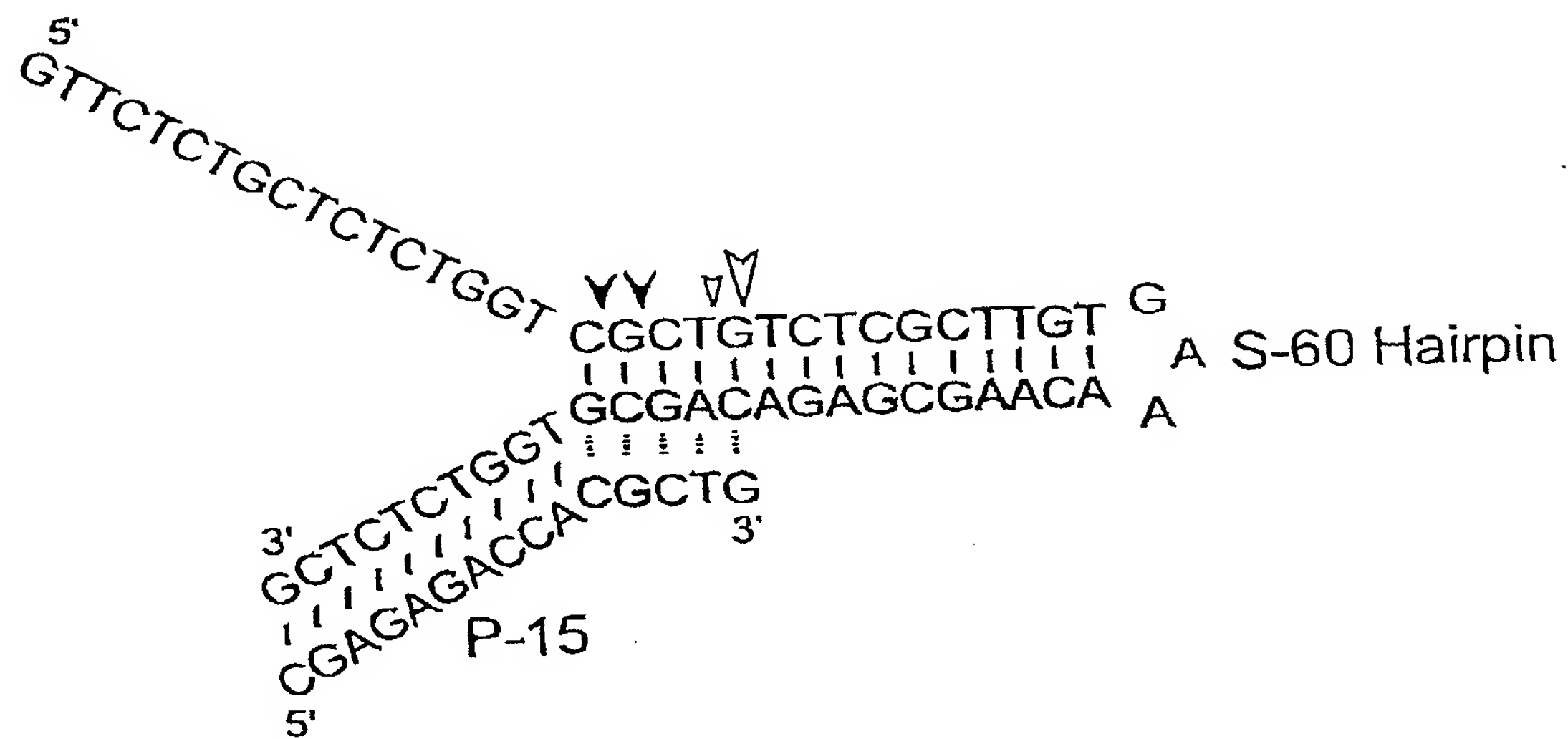


FIGURE 26



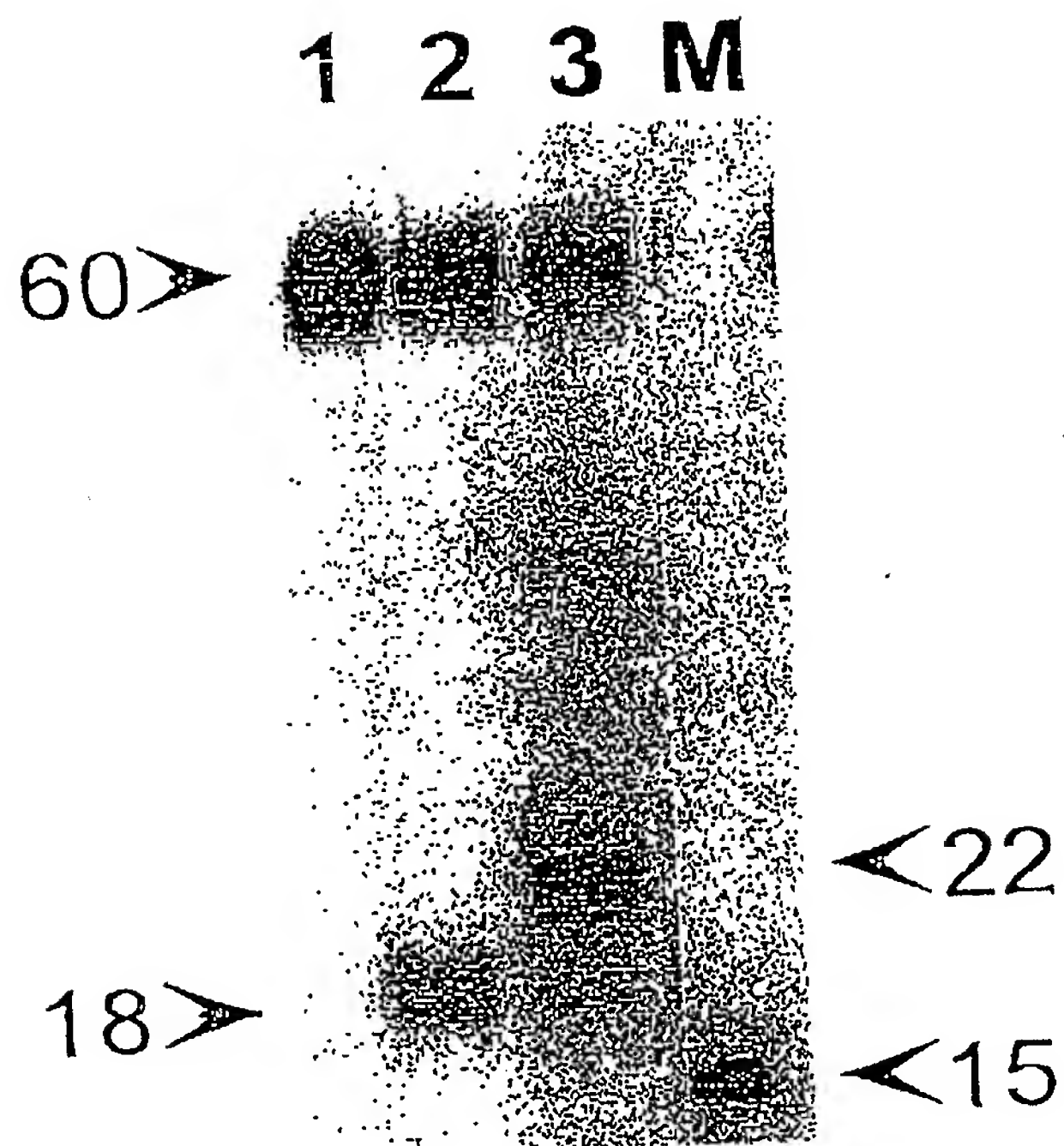


FIGURE 27

FIGURE 28

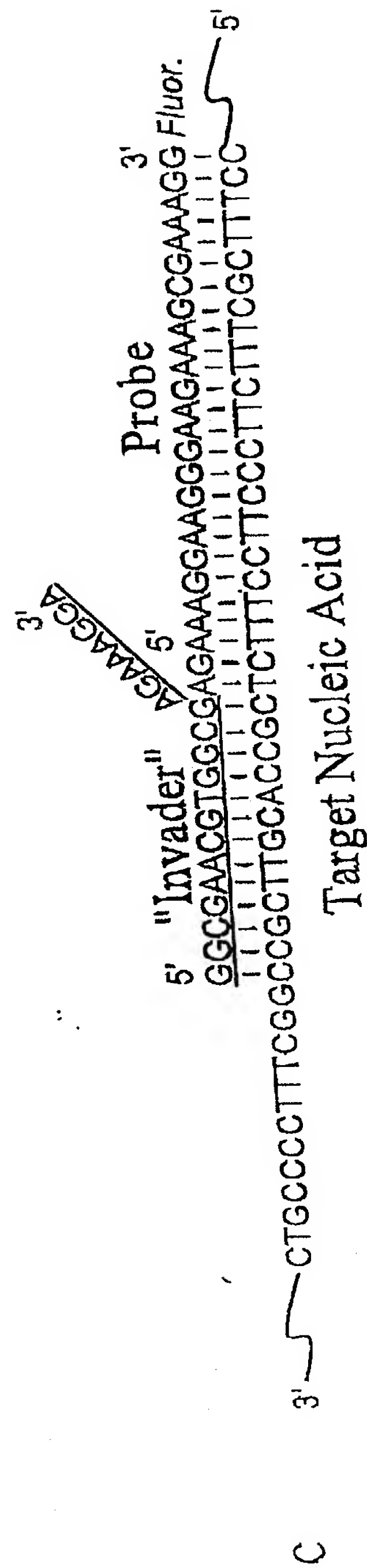
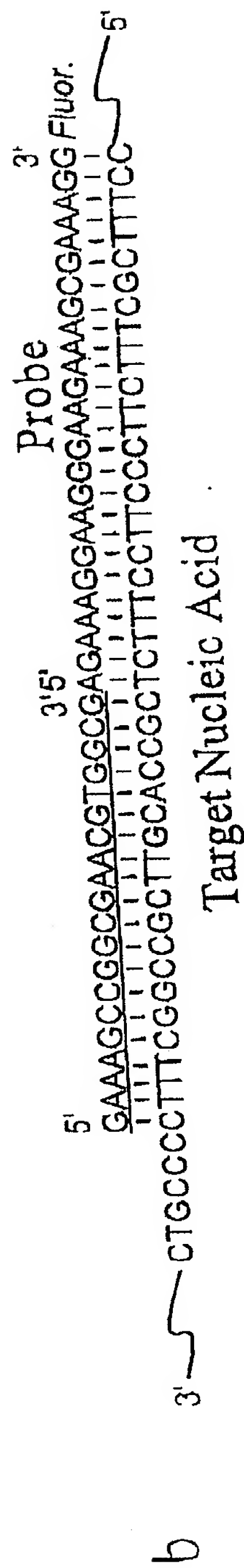
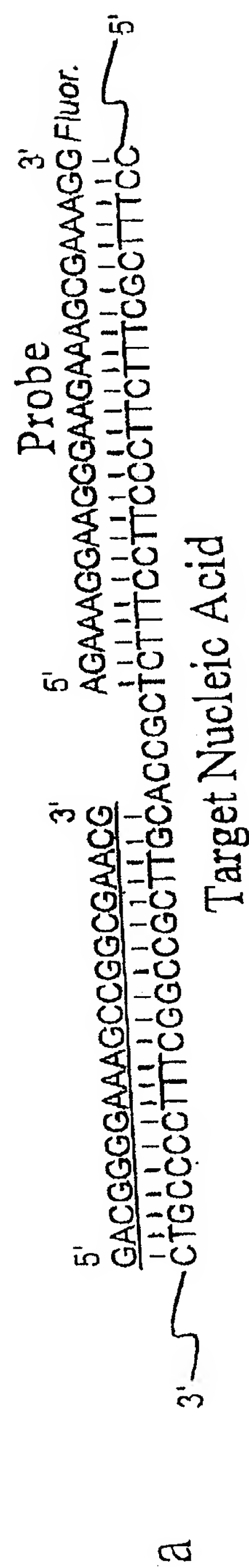
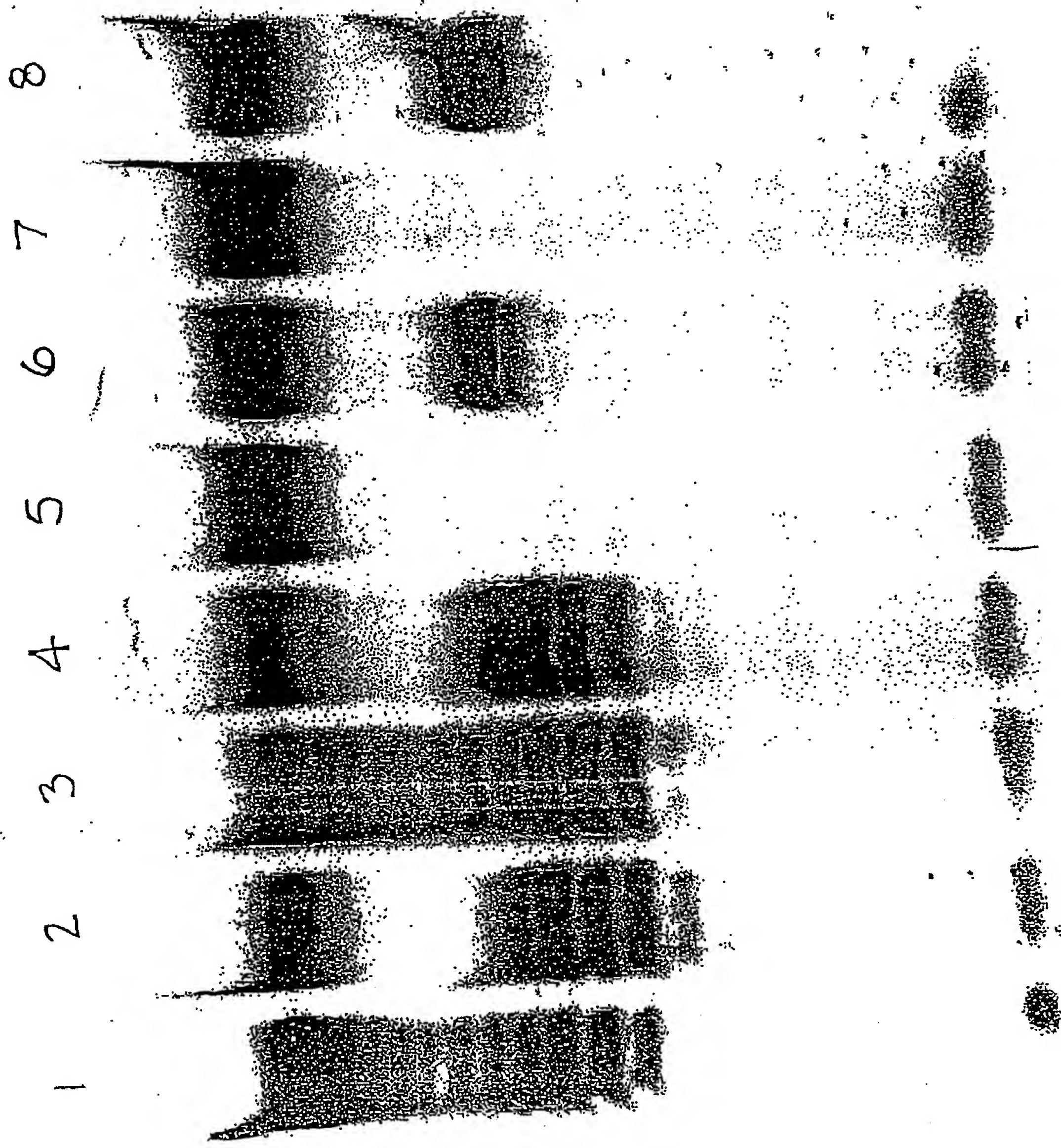


FIGURE 29



267

FIGURE 30

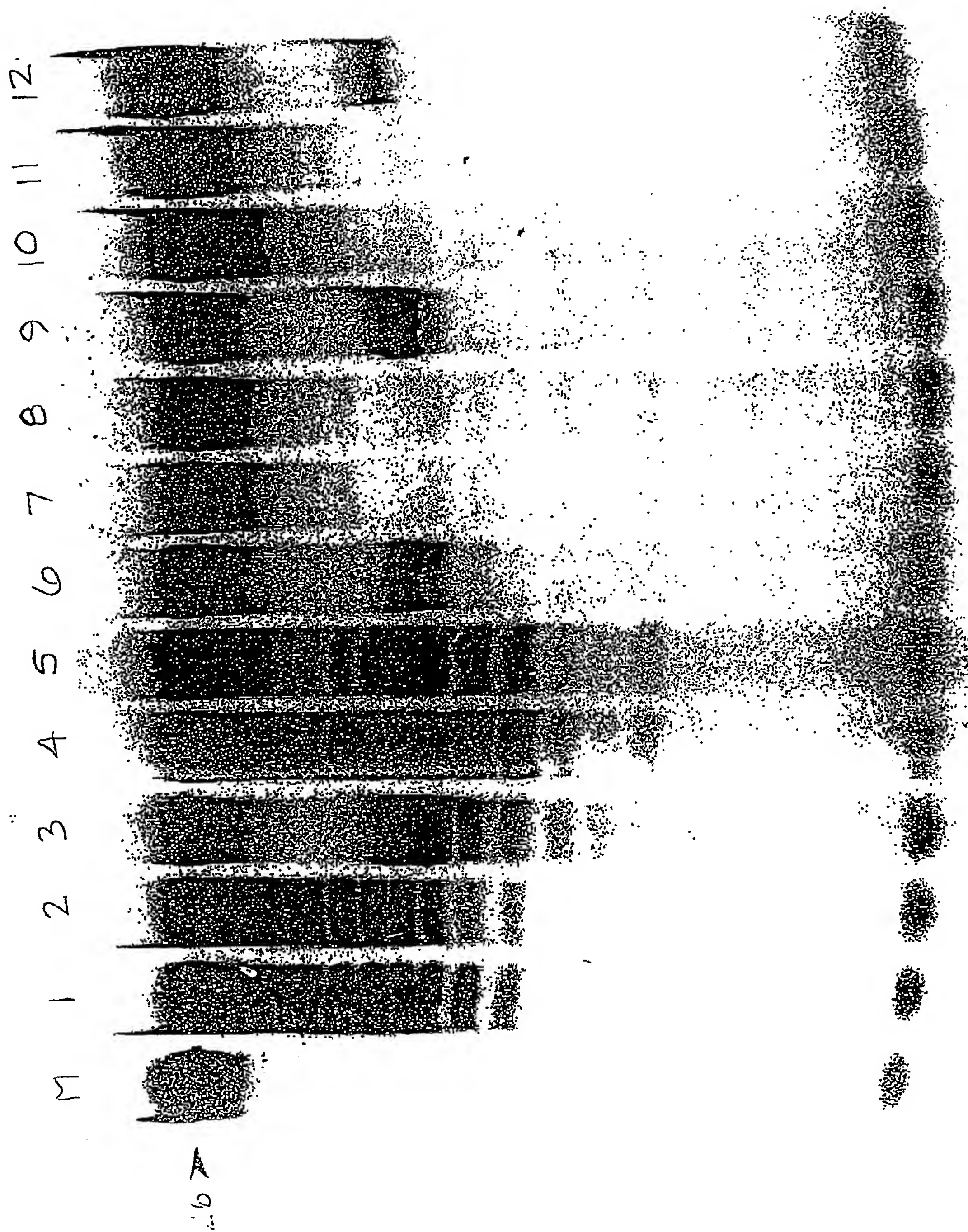


FIGURE 31

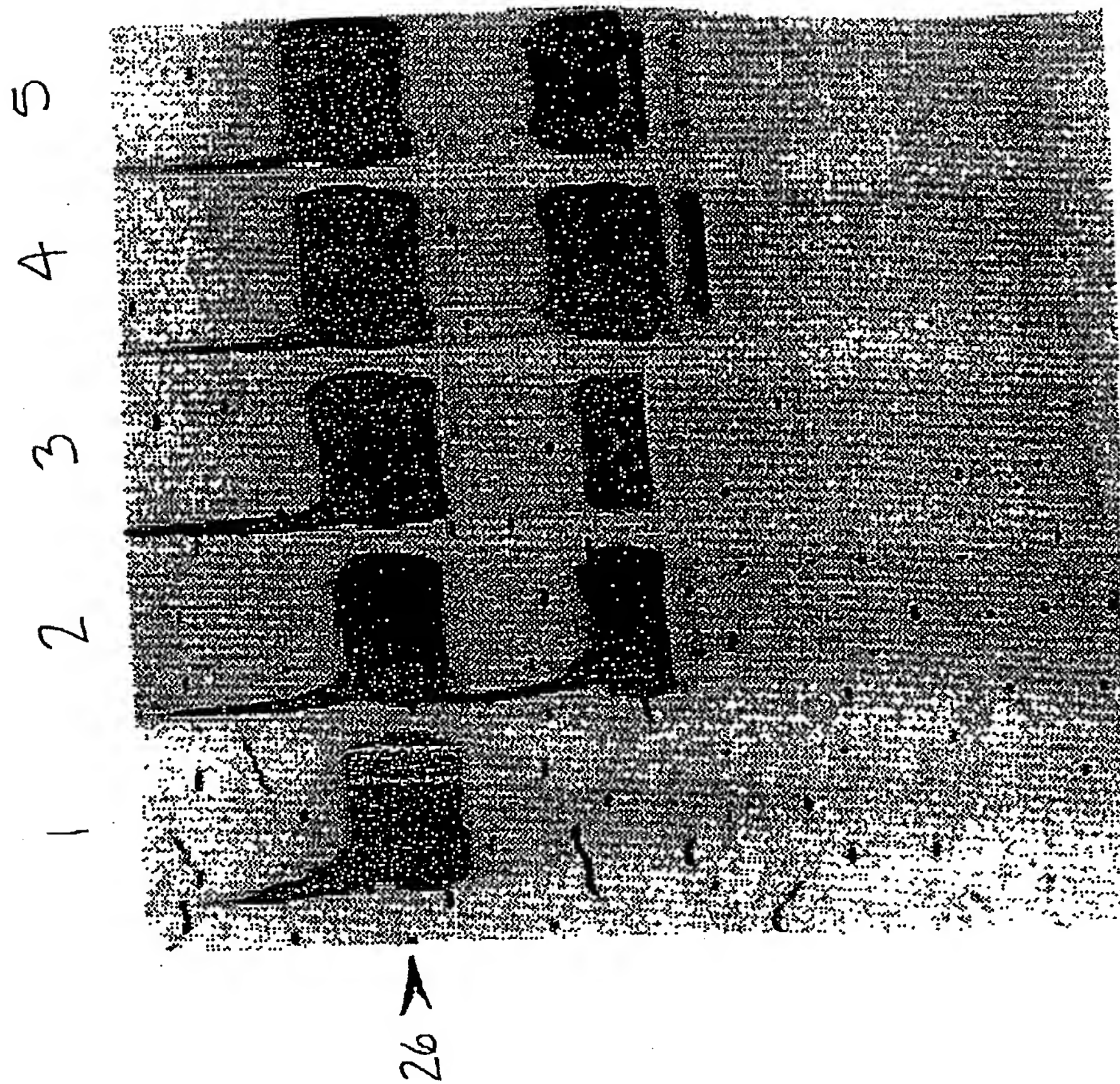


FIGURE 32

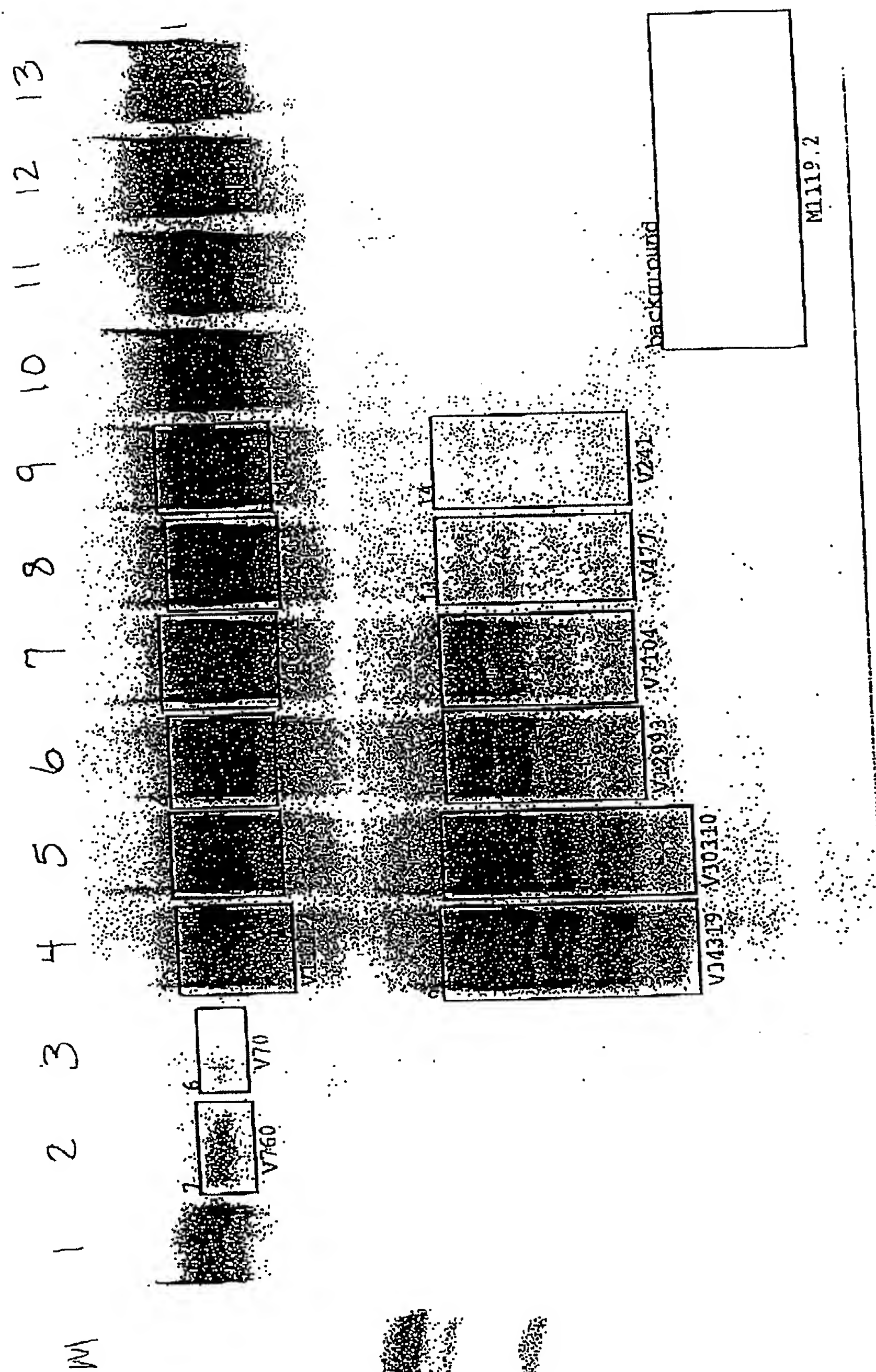


FIGURE 33

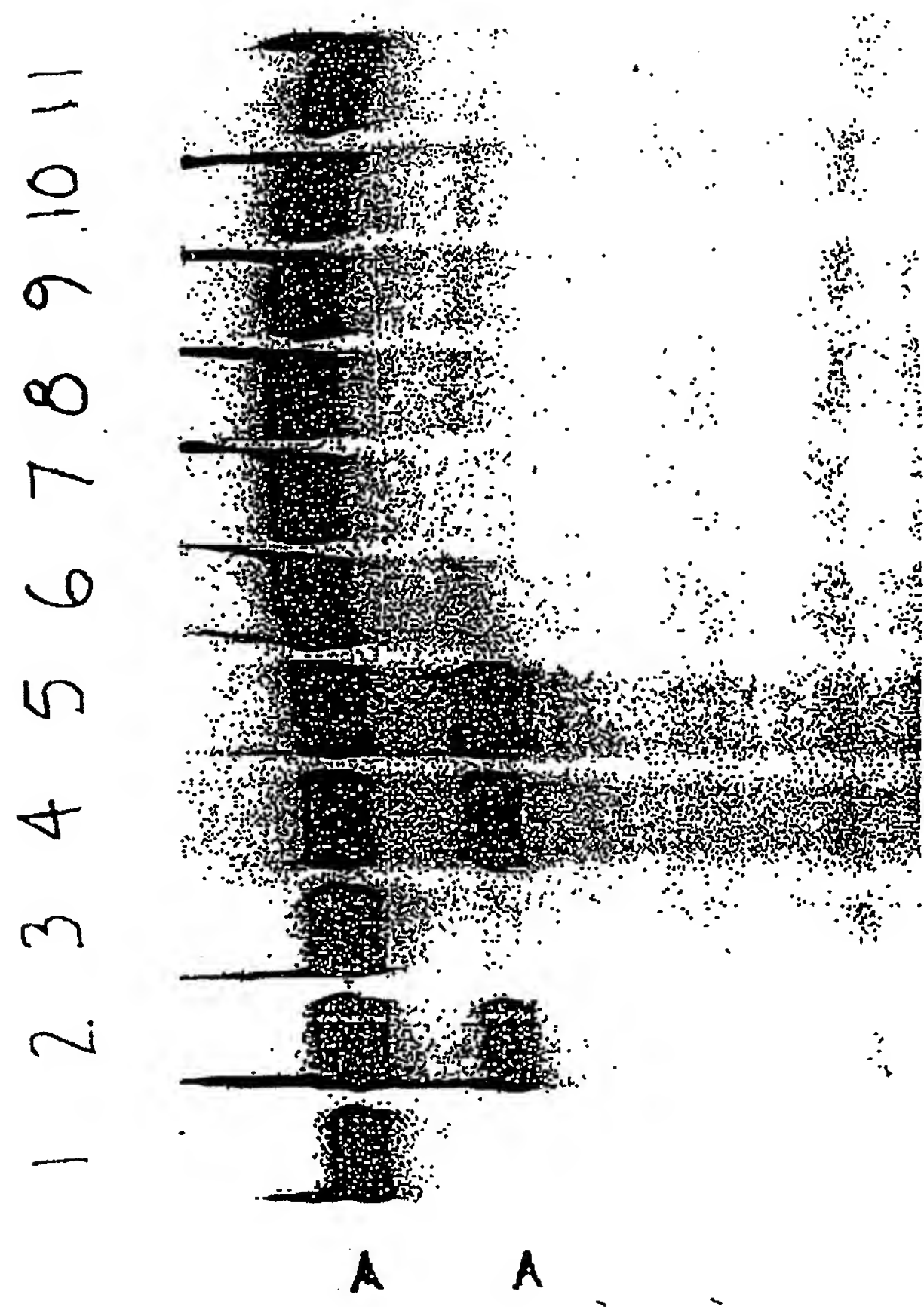


FIGURE 34

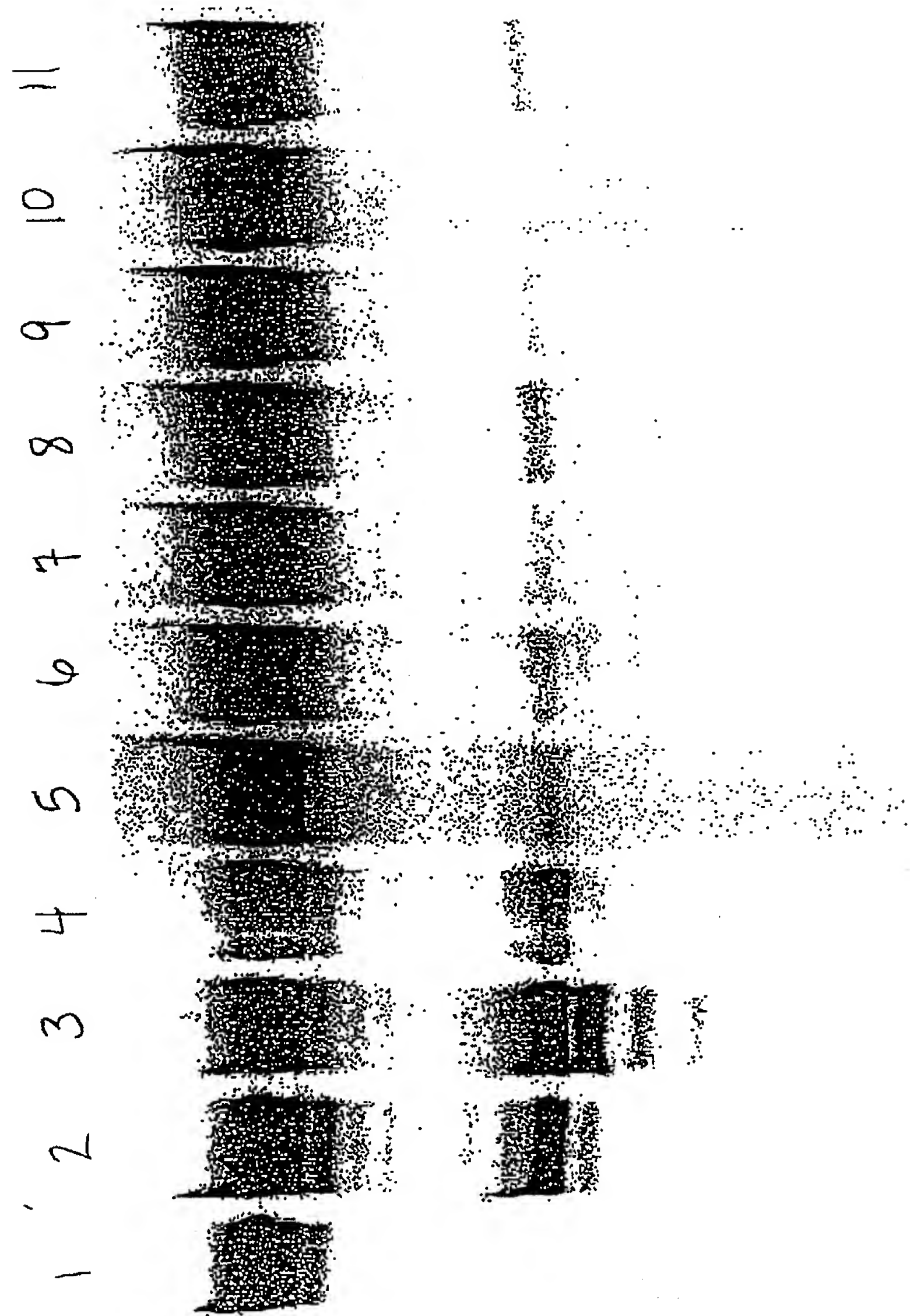
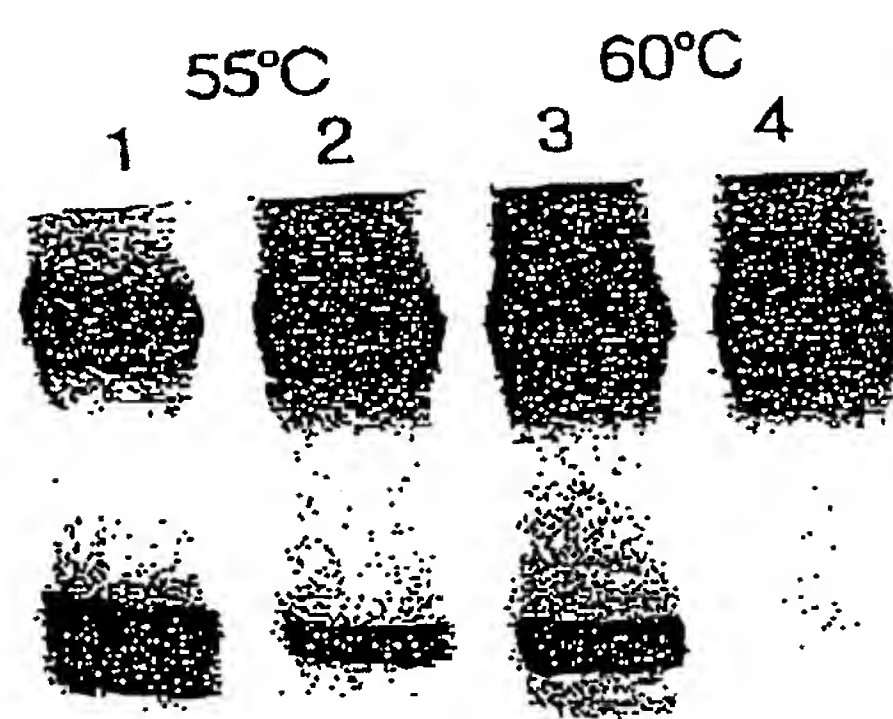


FIGURE 35



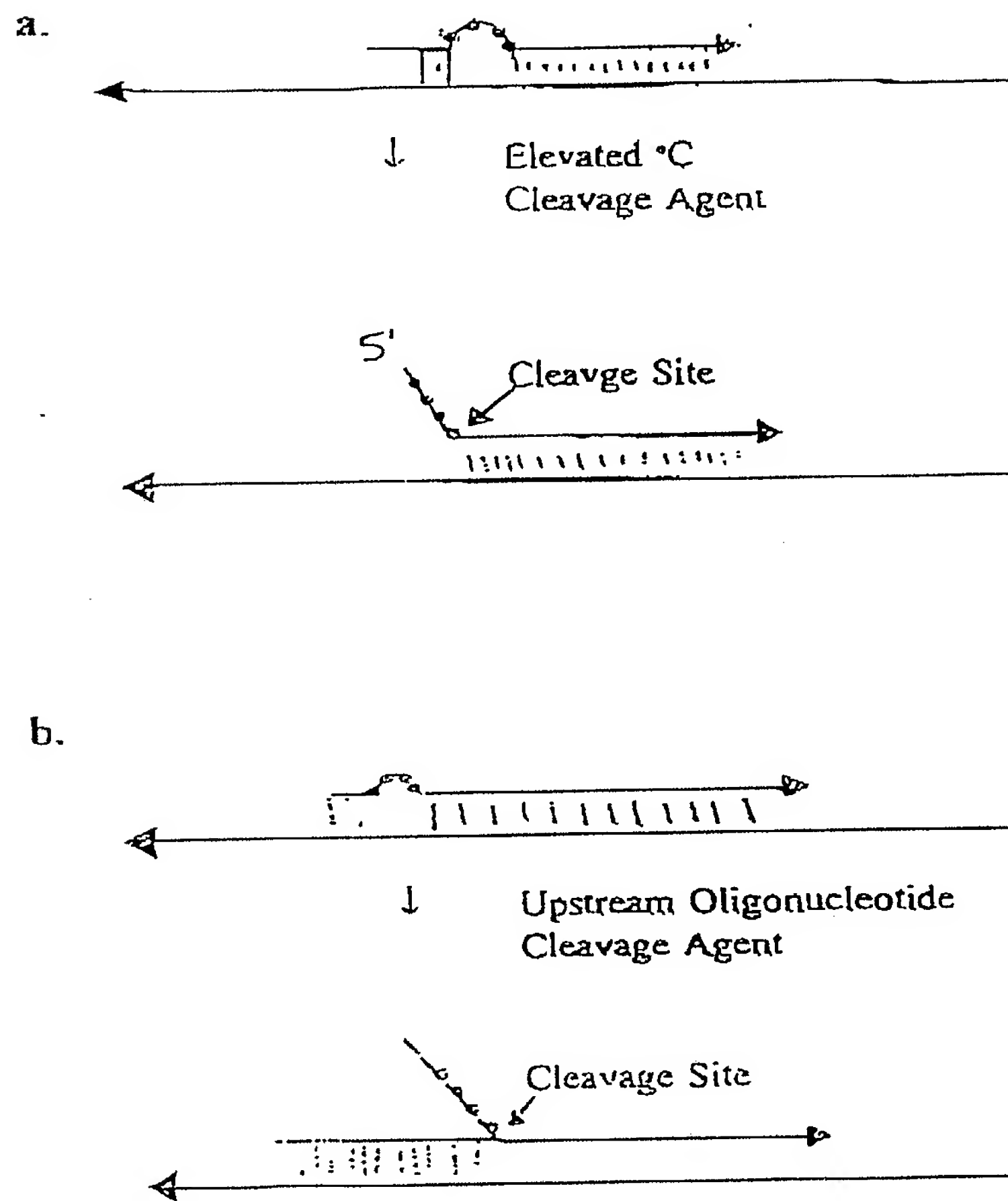


FIGURE 36

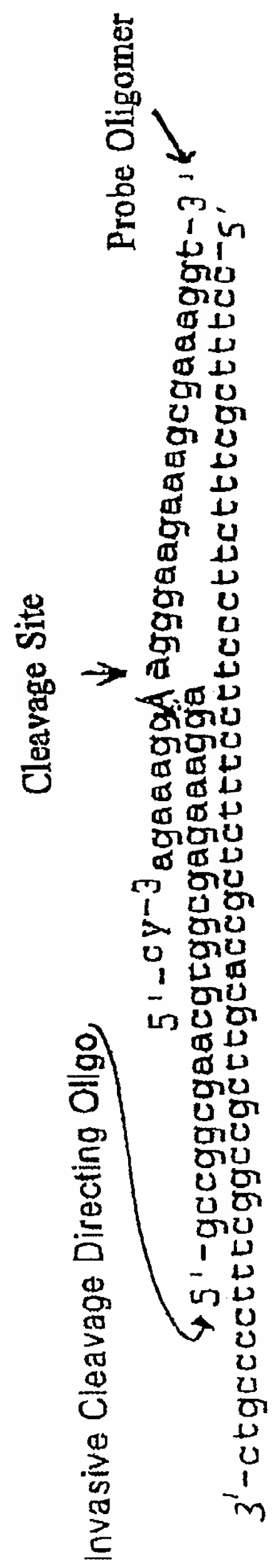


FIGURE 37

FIGURE 38

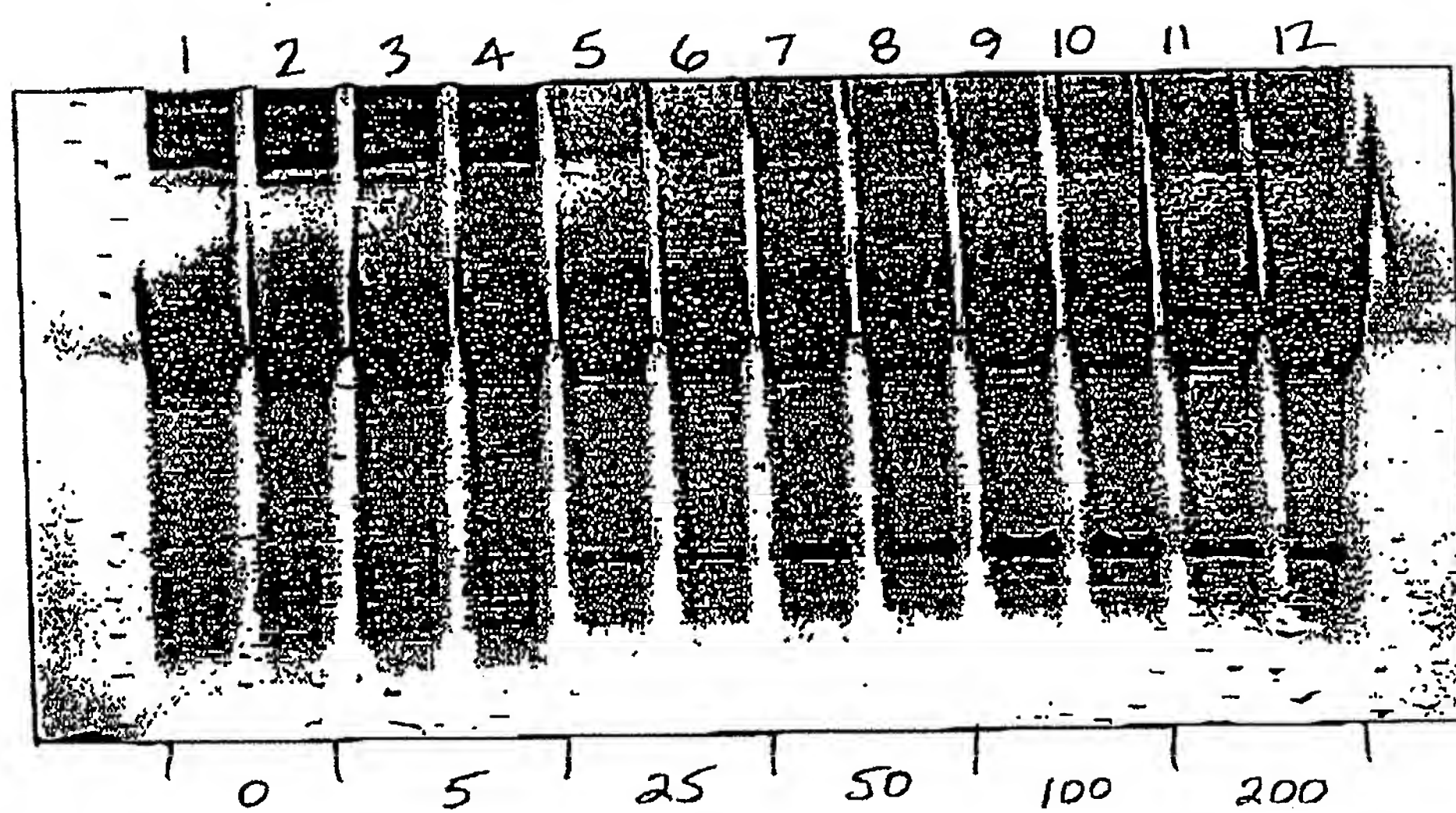


FIGURE 39

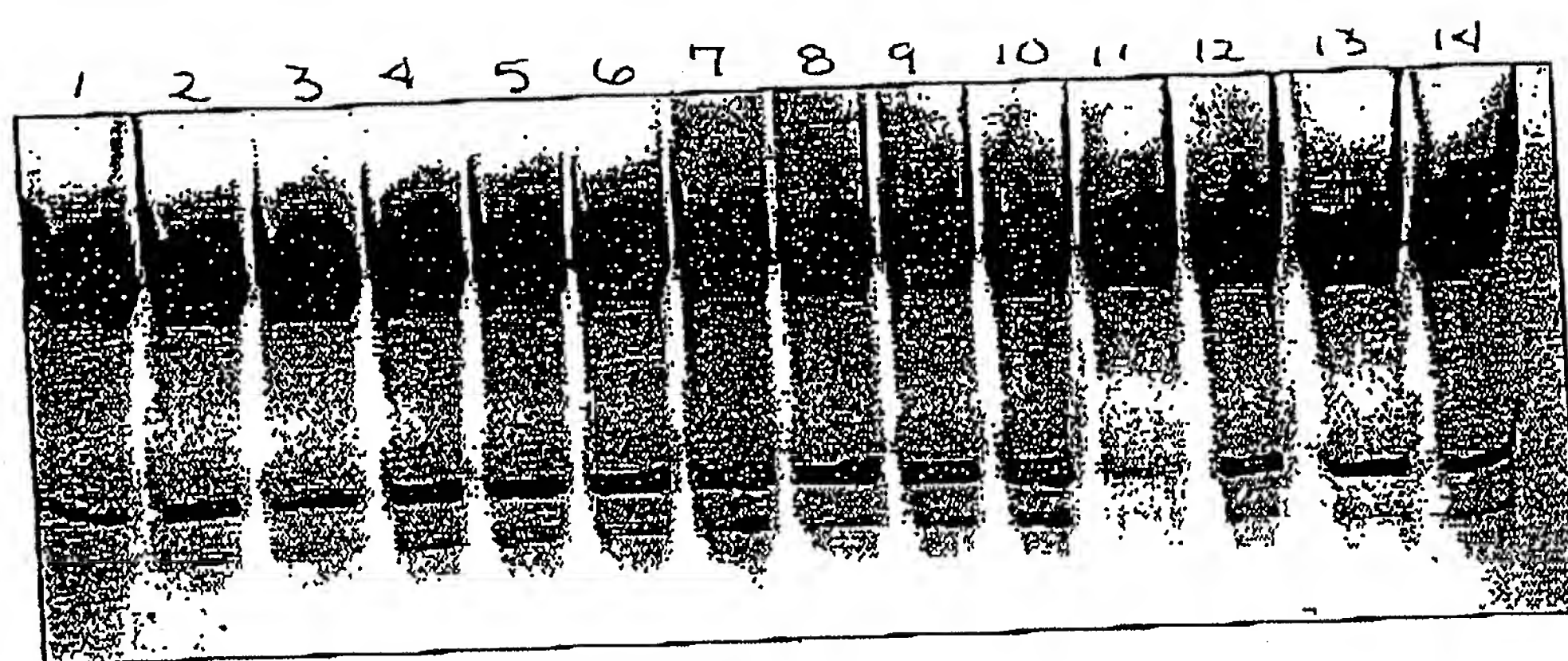


FIGURE 40

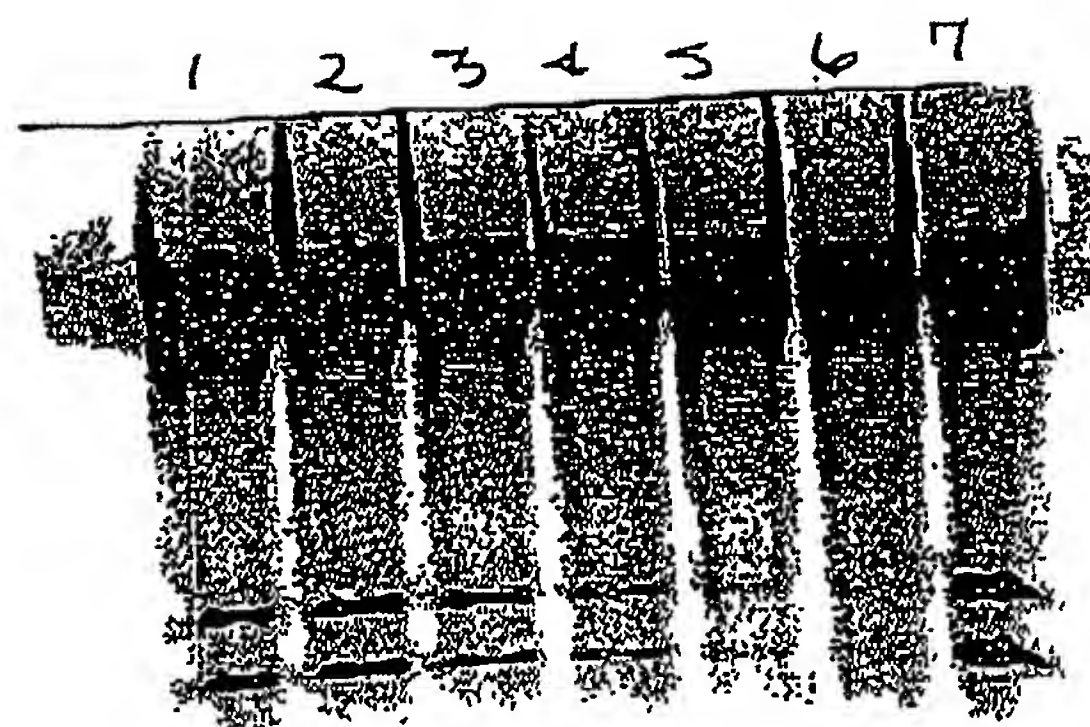


FIGURE 41

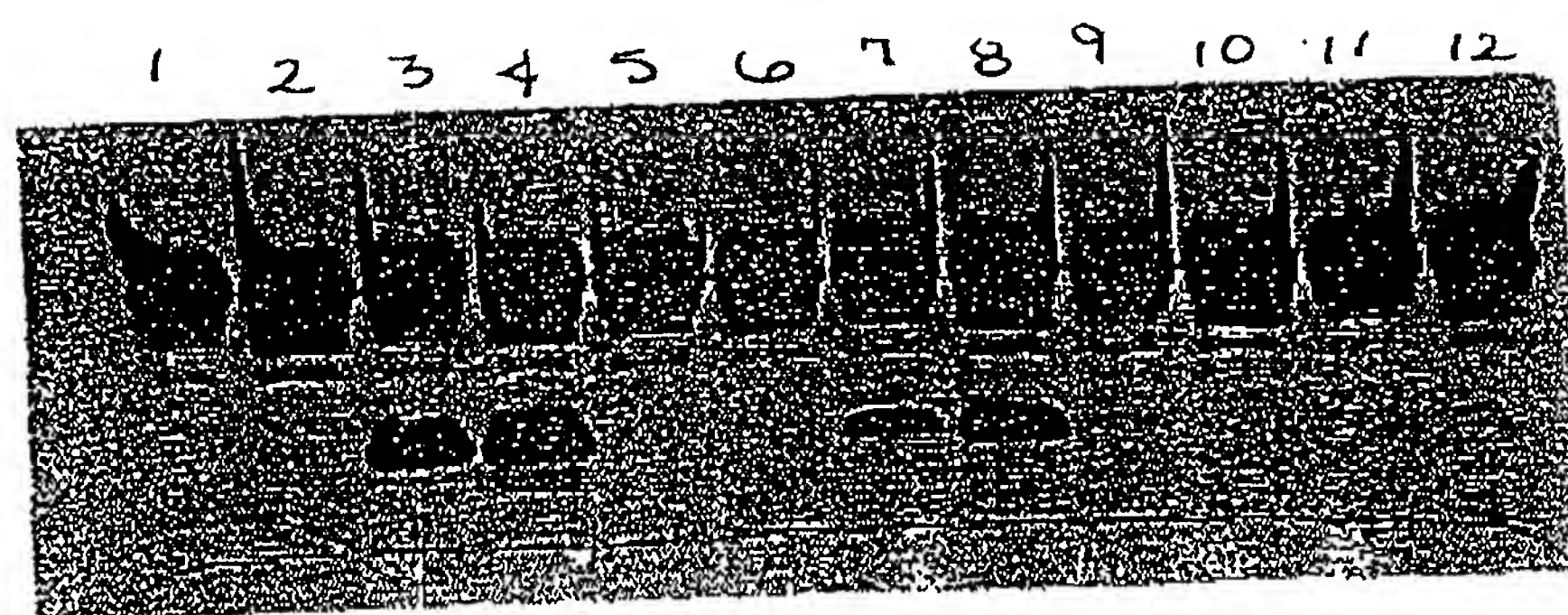


FIGURE 42A

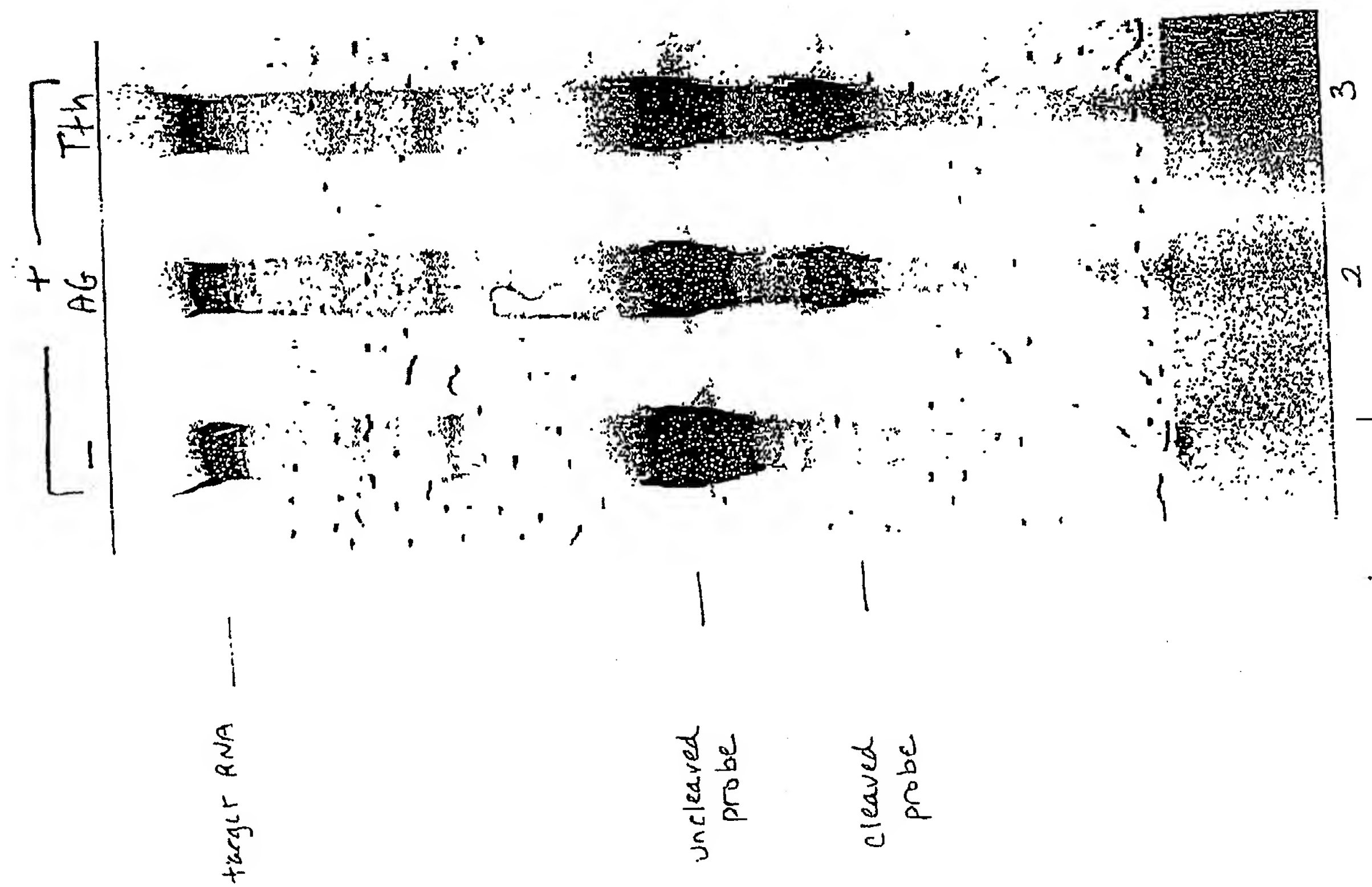
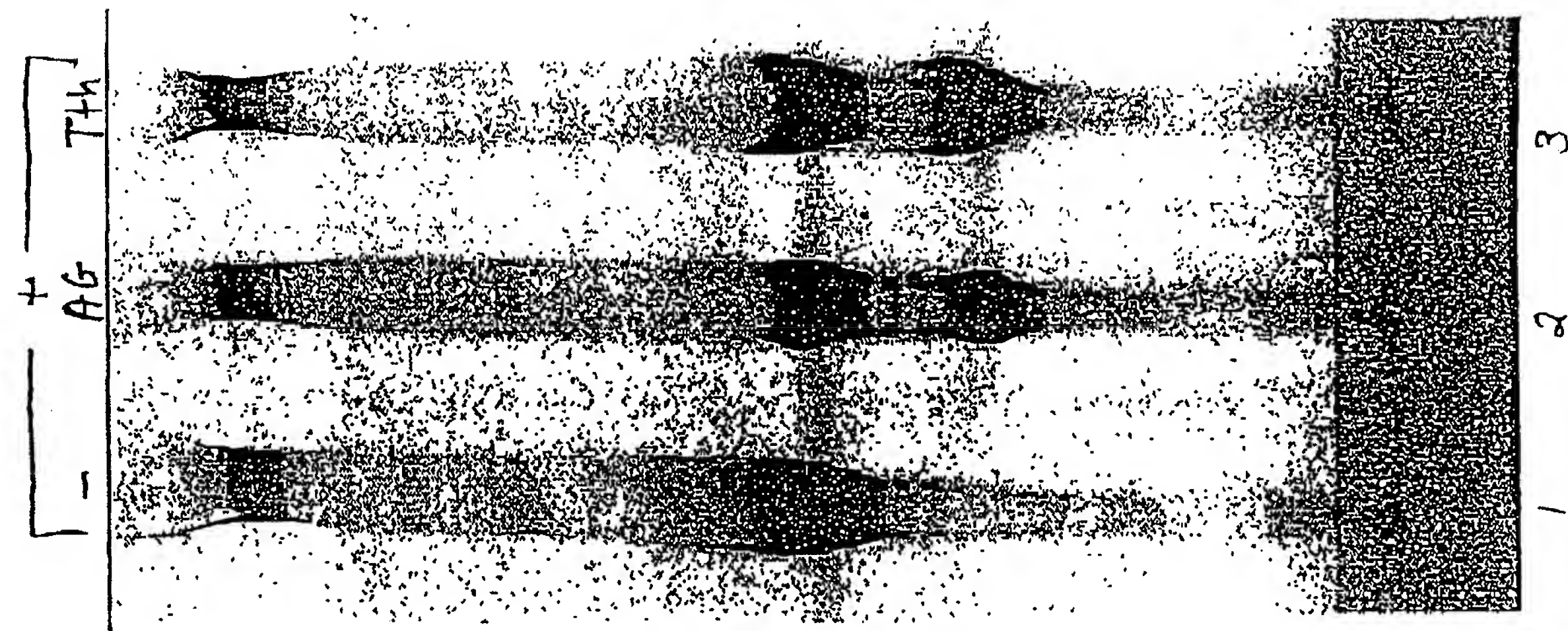


FIGURE 42B



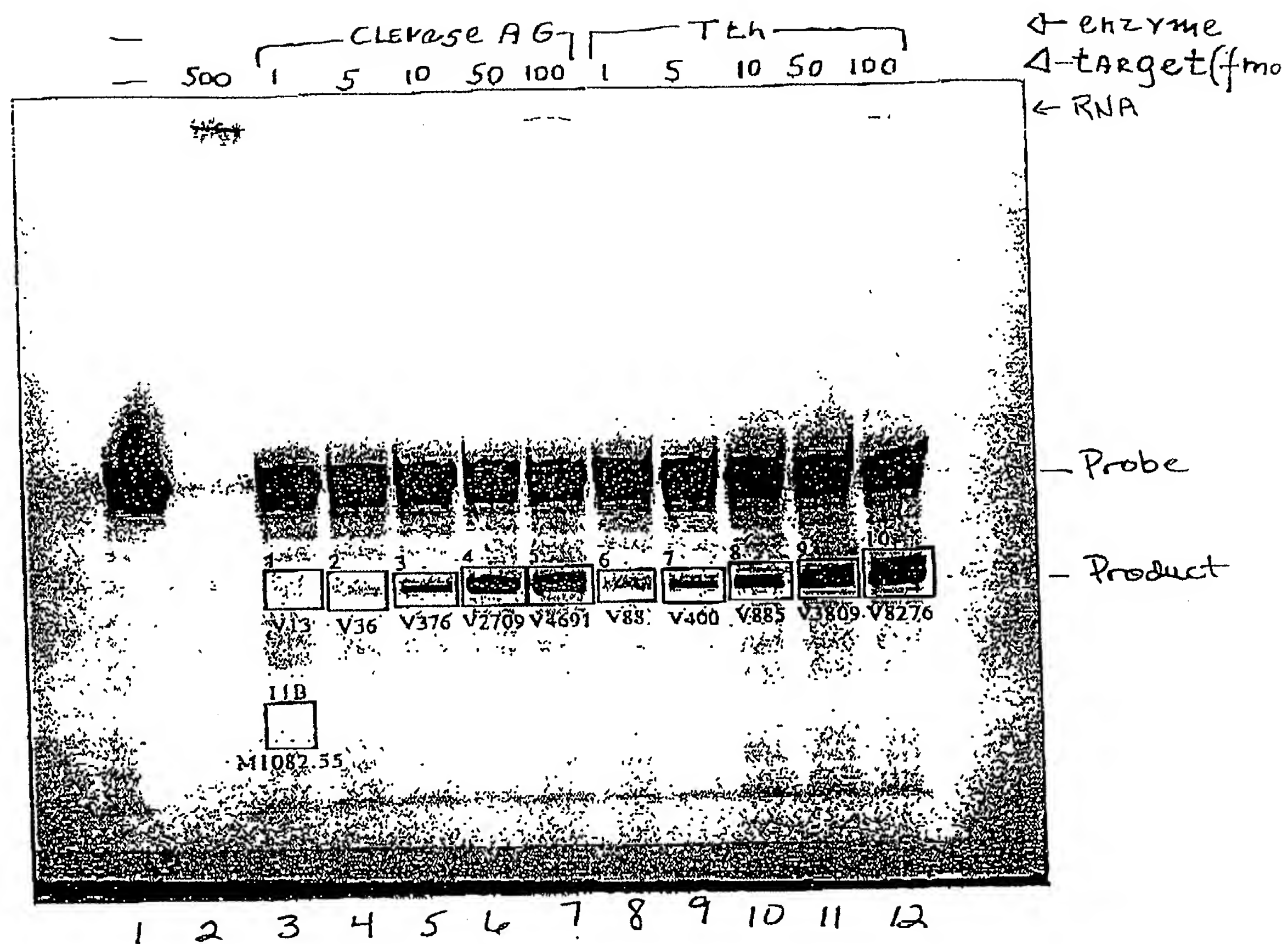


FIGURE 43

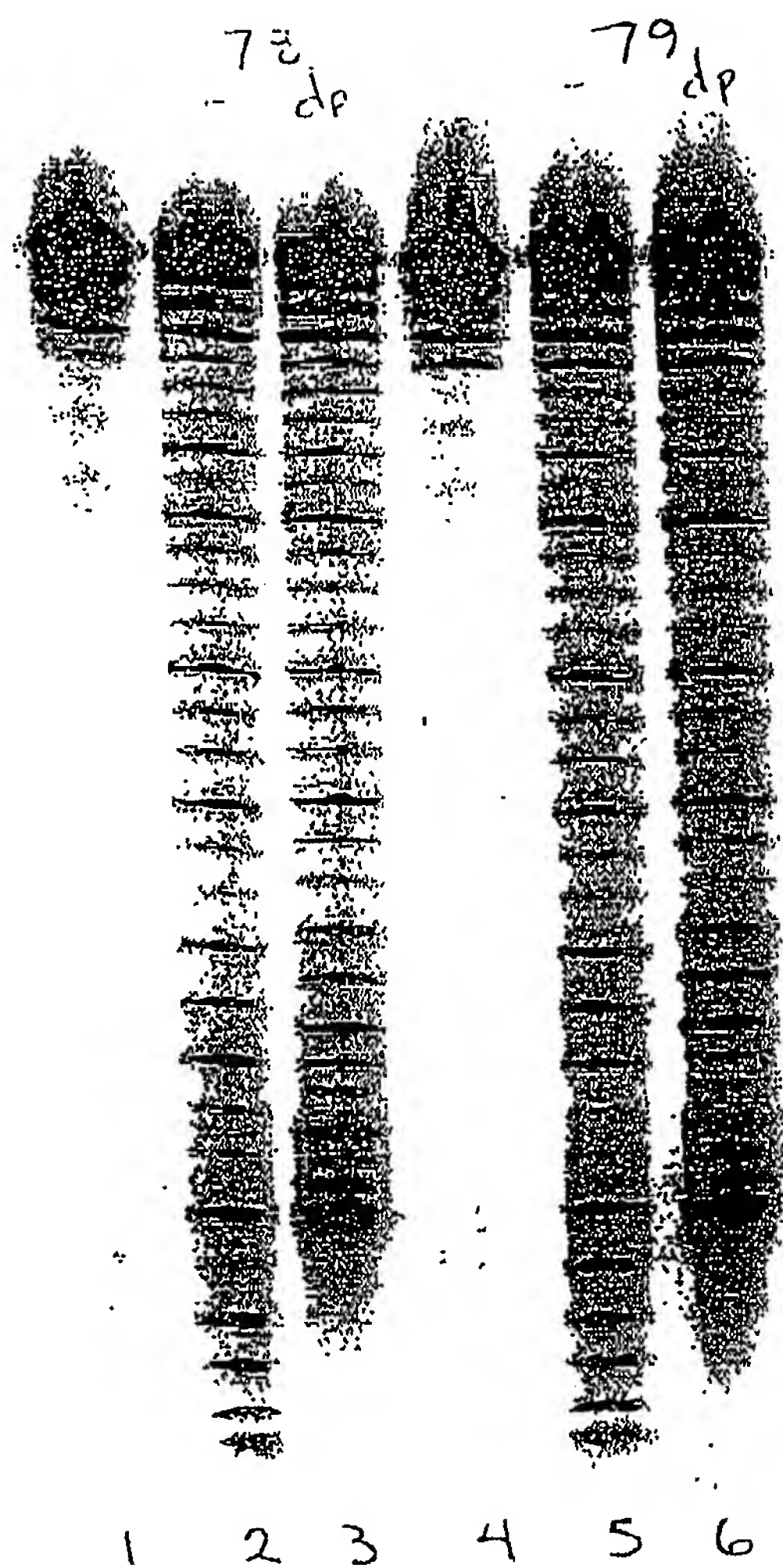


FIGURE 44

FIGURE 45

70 (C10 aminoT's)

74 (C6 amino T's)

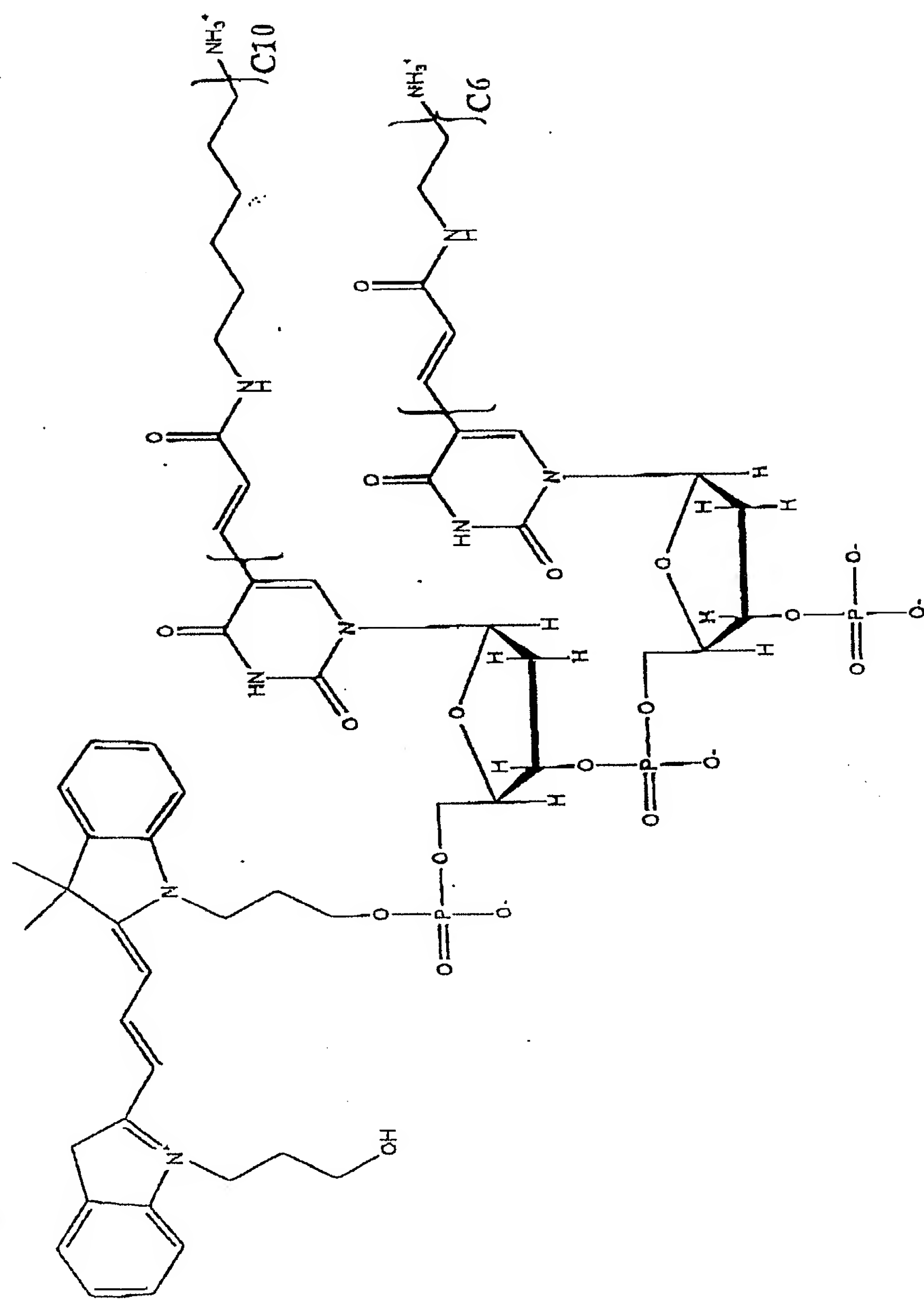


FIGURE 46

75

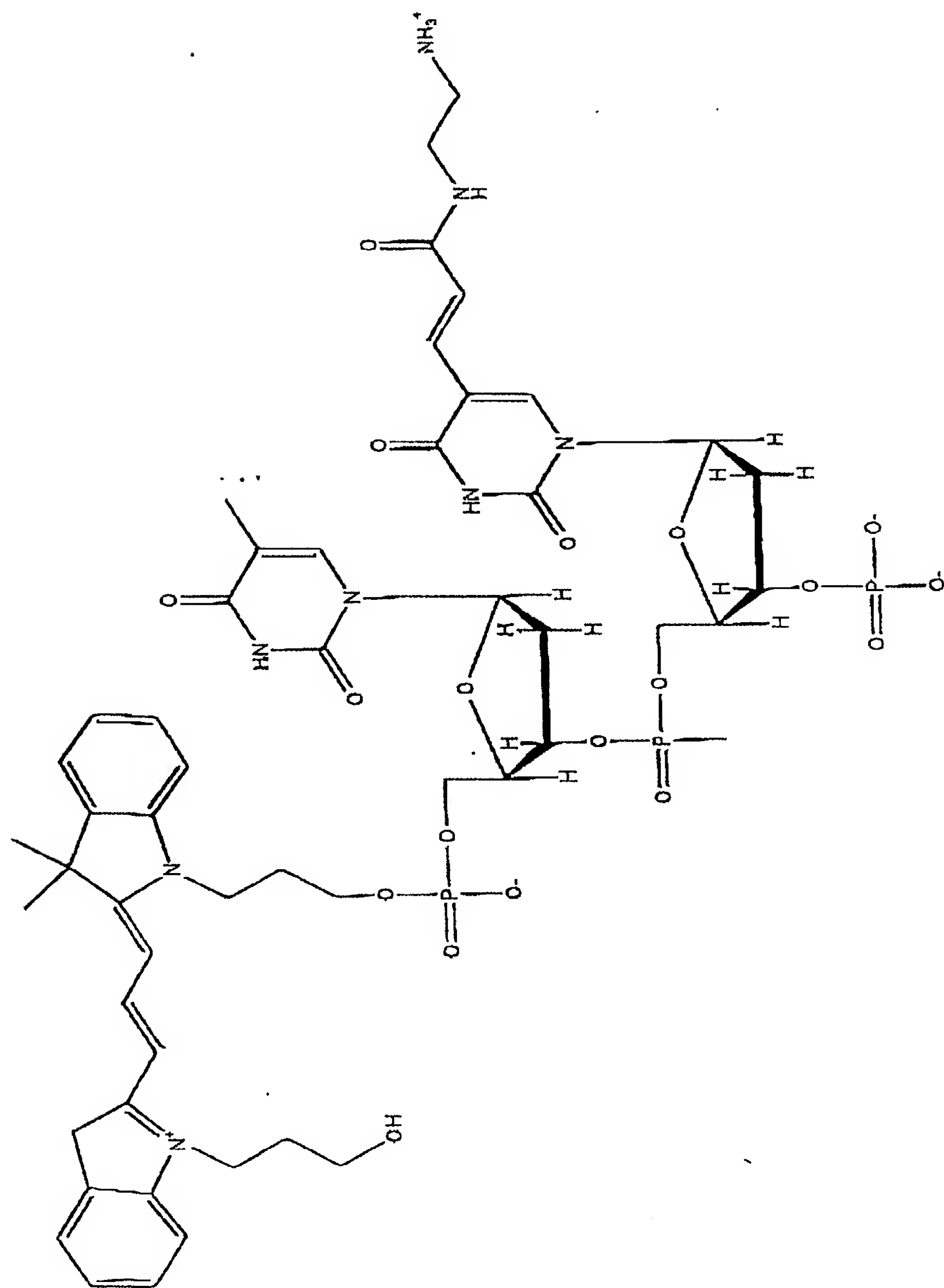


FIGURE 47

76

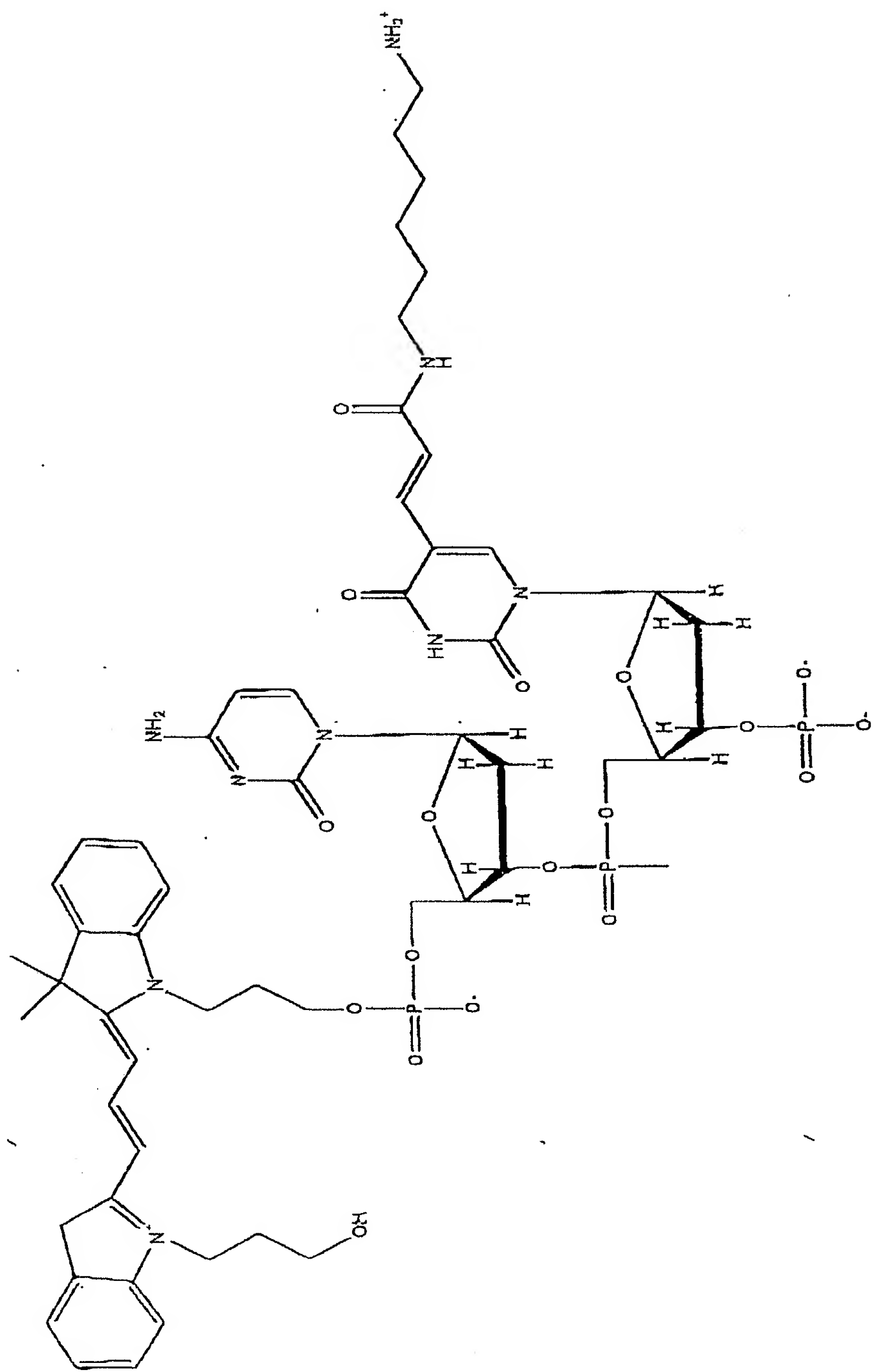
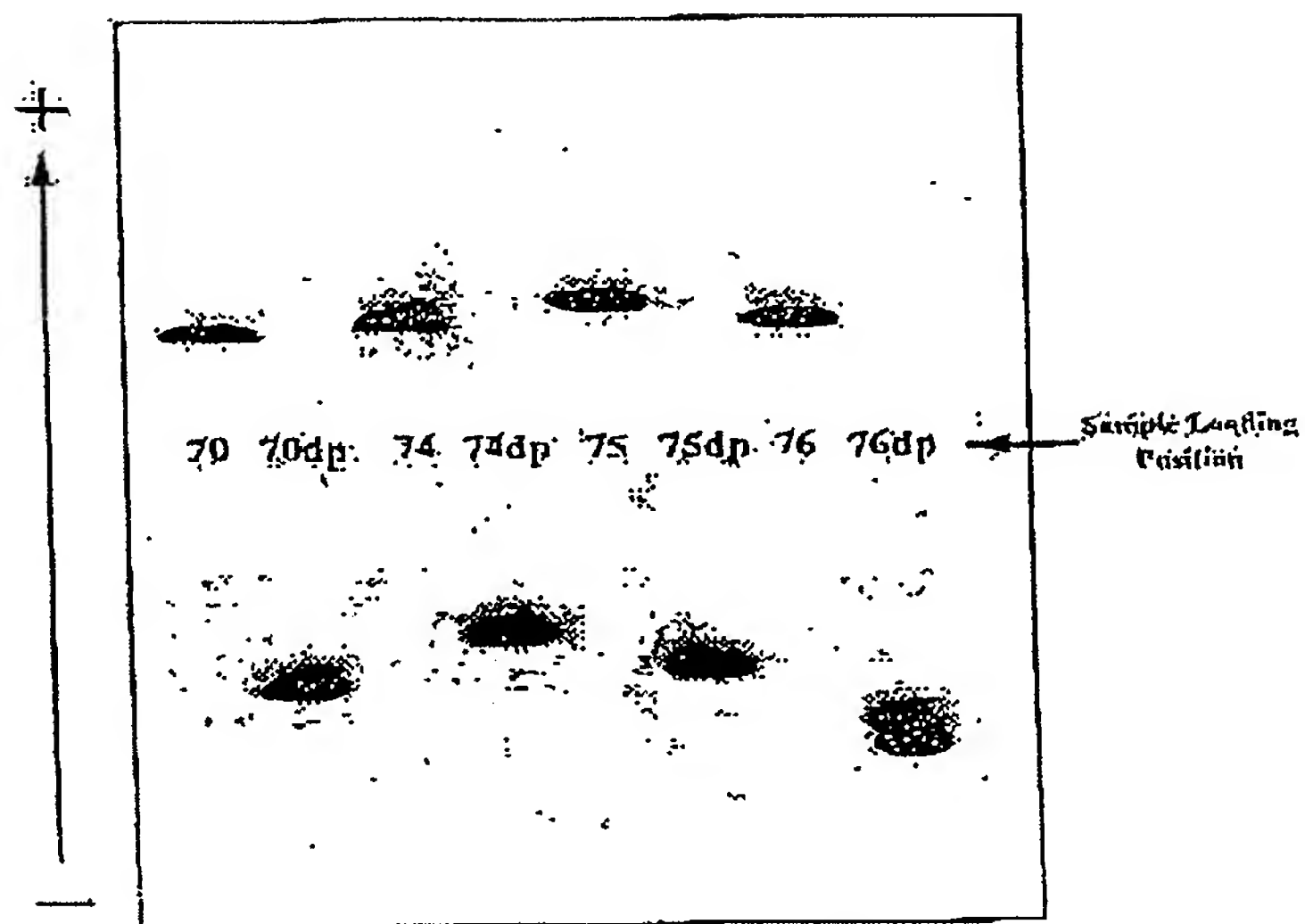
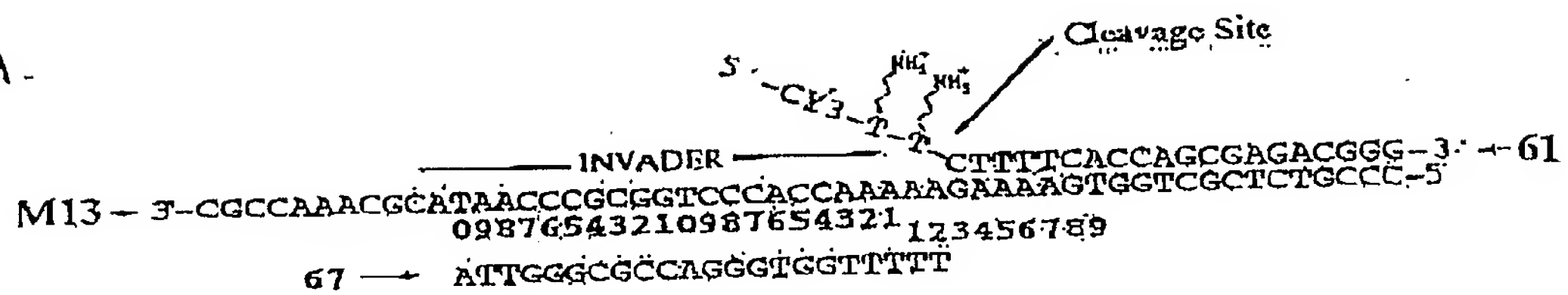


FIGURE 48



A.



B.

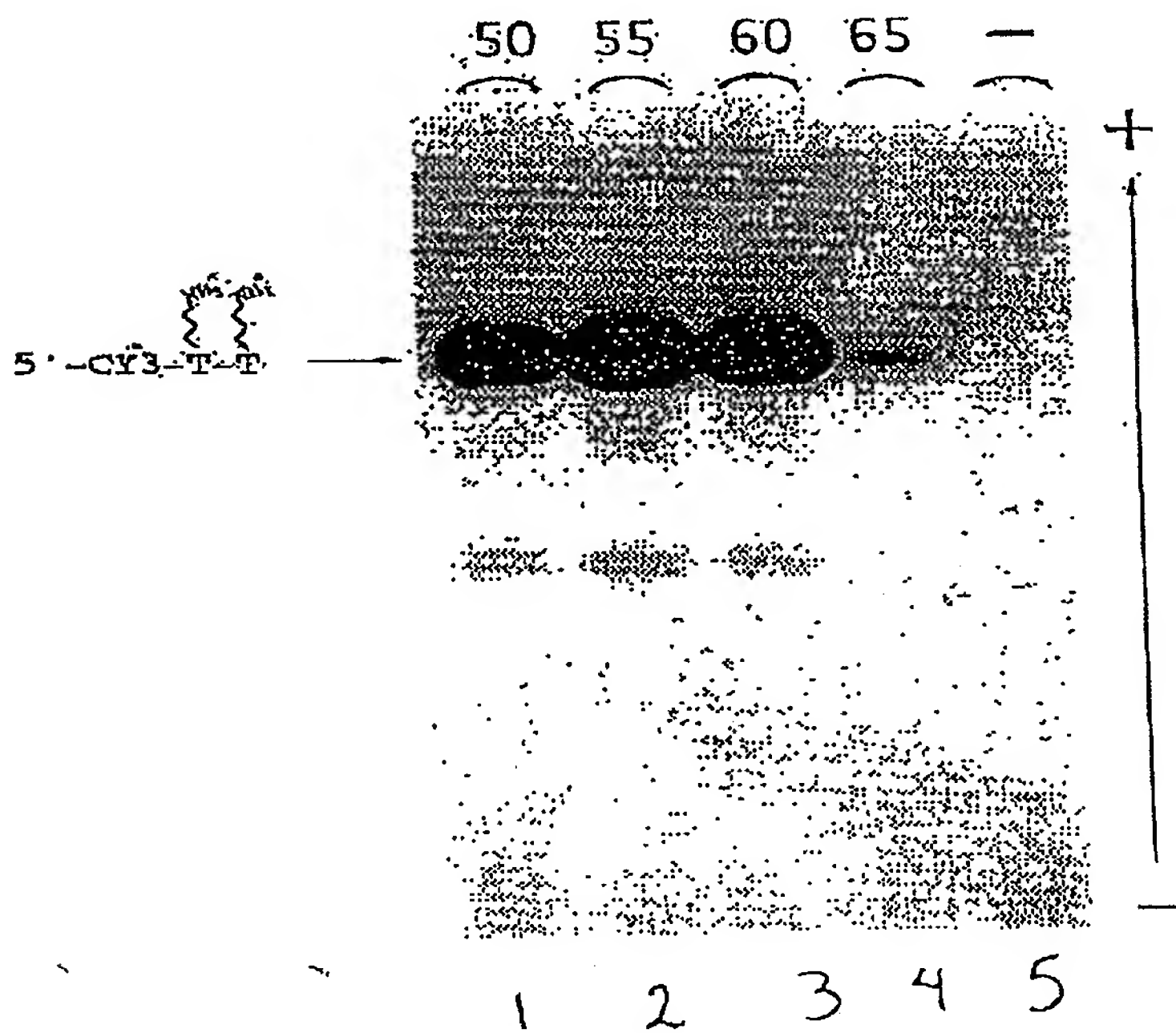


FIGURE 49

FIGURE 50

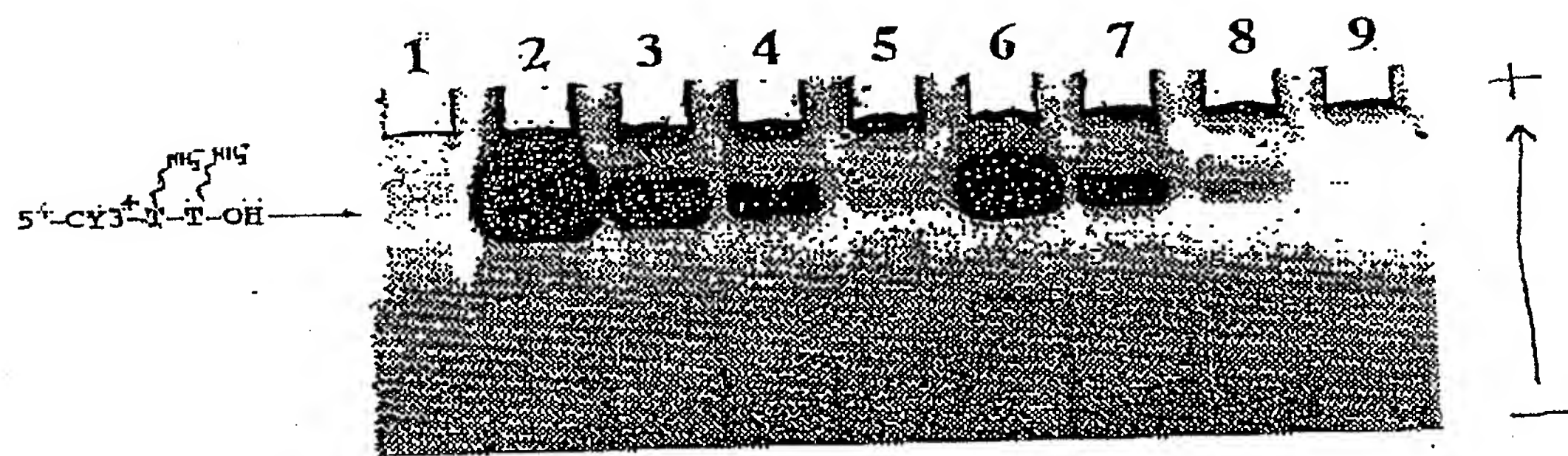


FIGURE 51

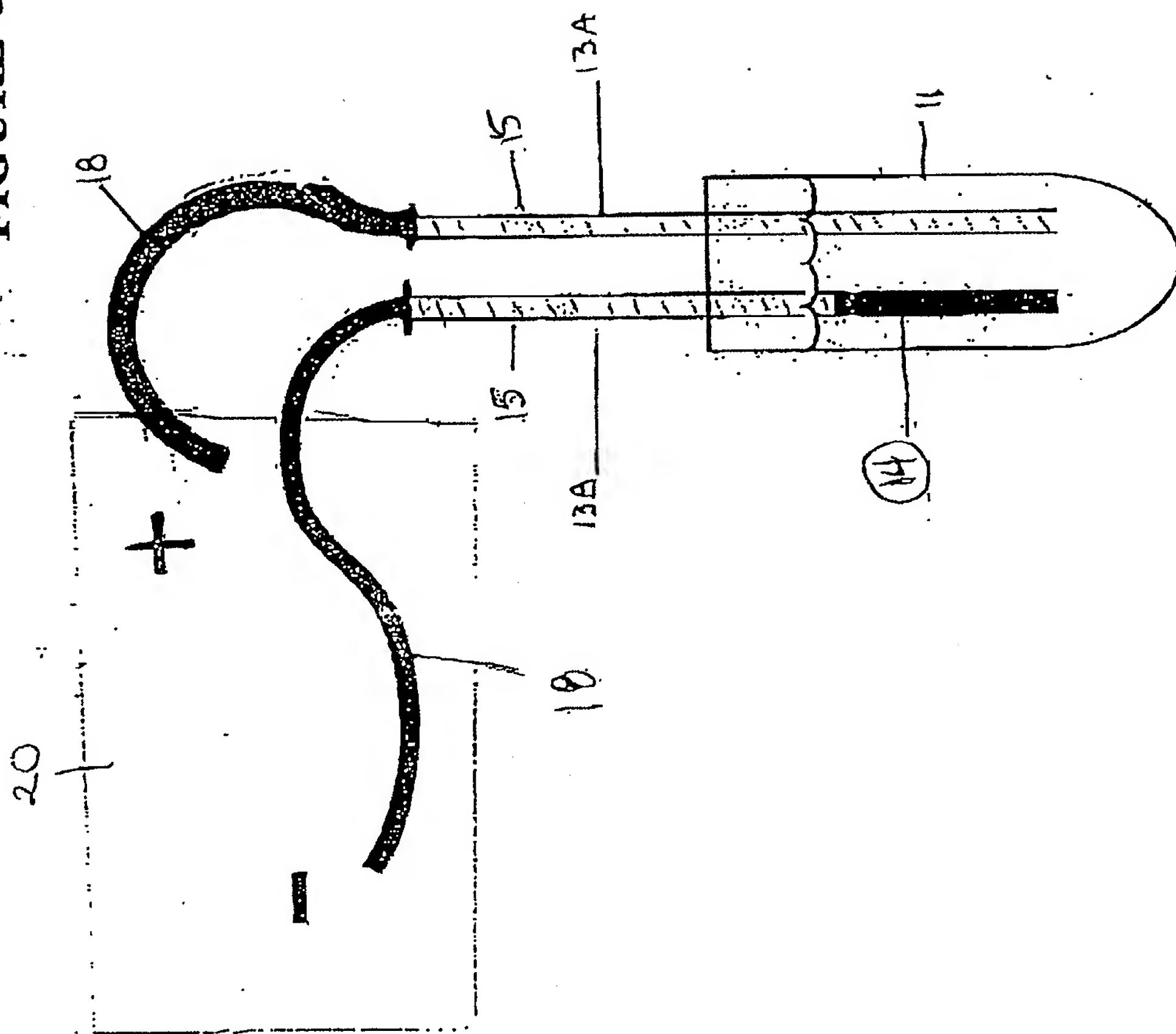


FIGURE 52

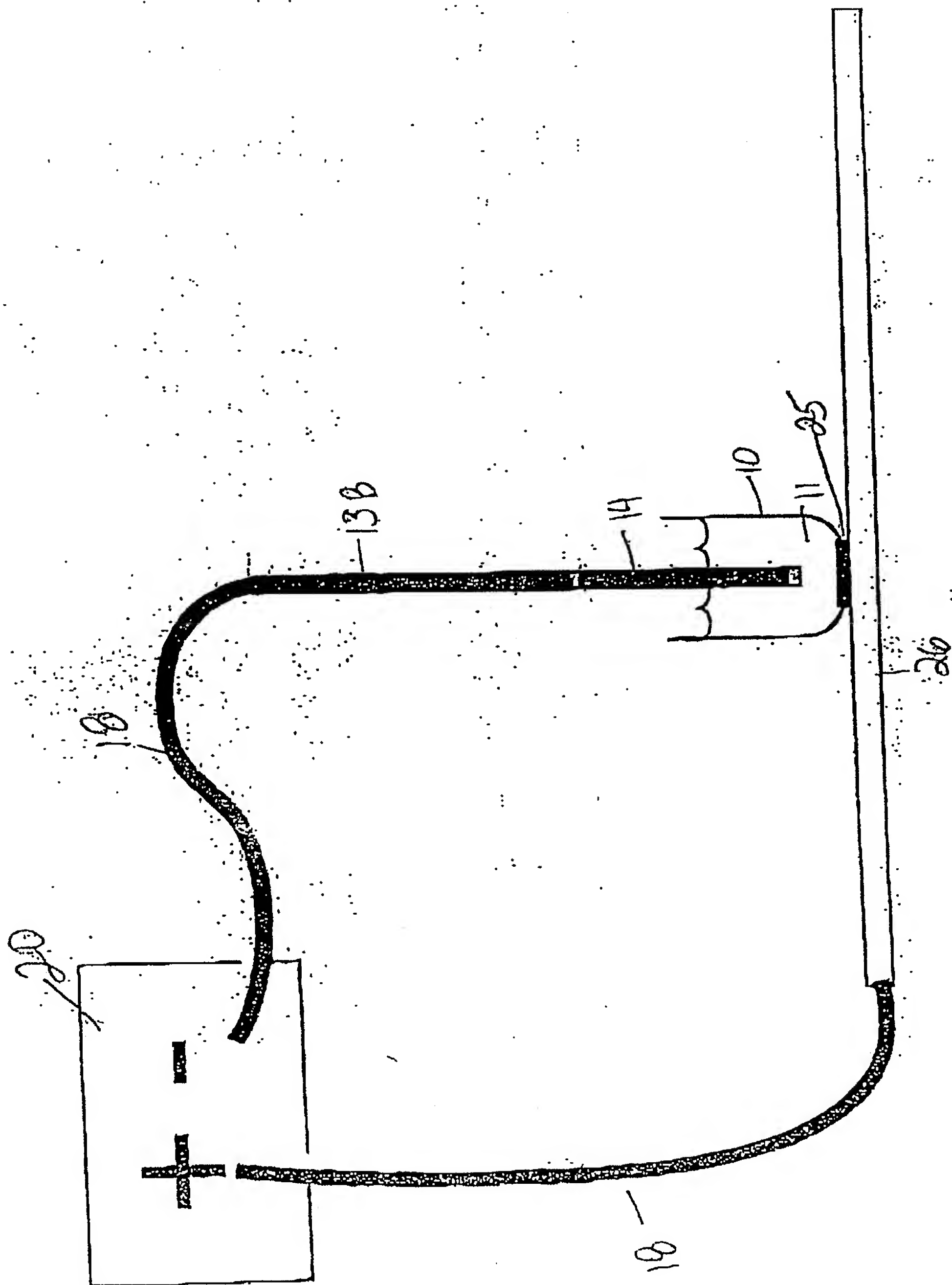
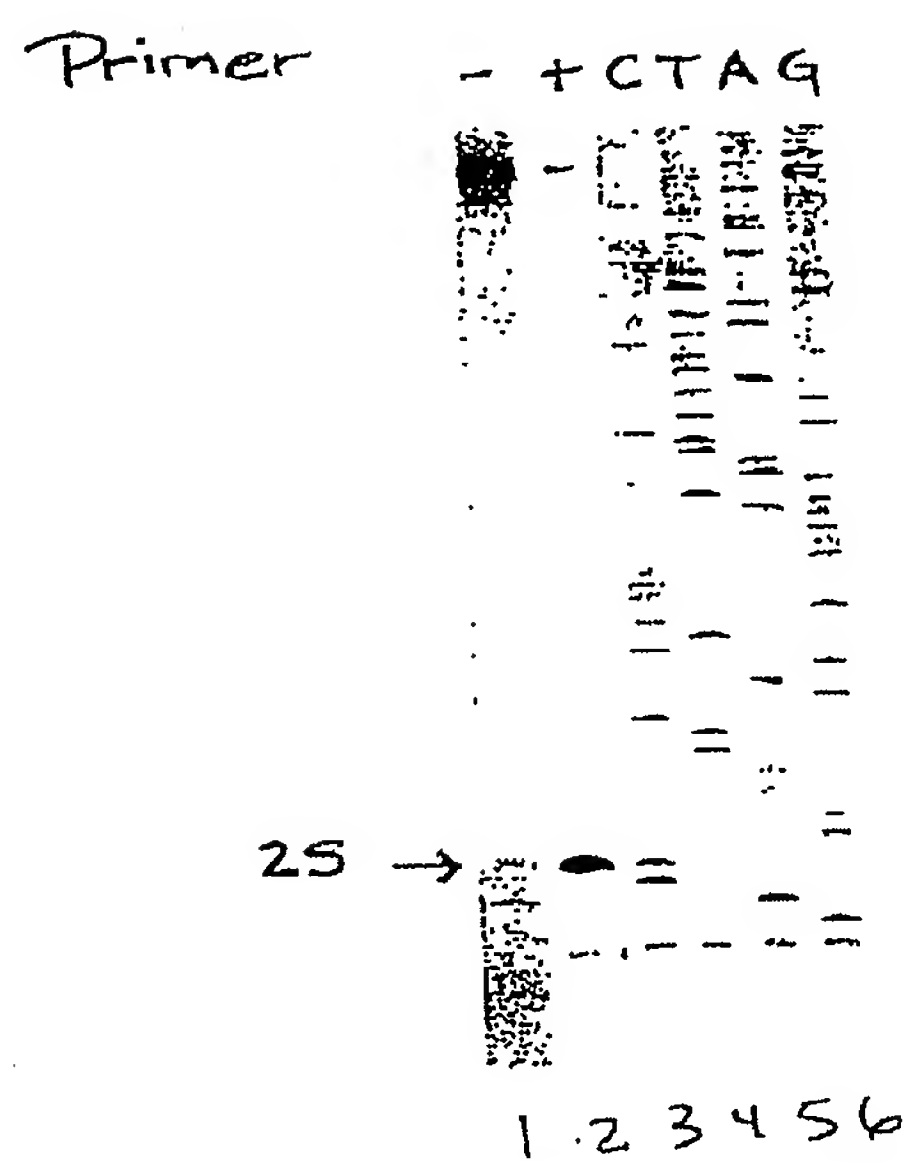


FIGURE 53



5' ▼ AGAAAGGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

AGAAAGGA▼

5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

a

5' ▼ CAG AAGGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

CAGAAGGA▼

5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

b

5' ▼ CAGGG GGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

CAGGGGGA▼

5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

c

5' ▼ CAGGGTAC AGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

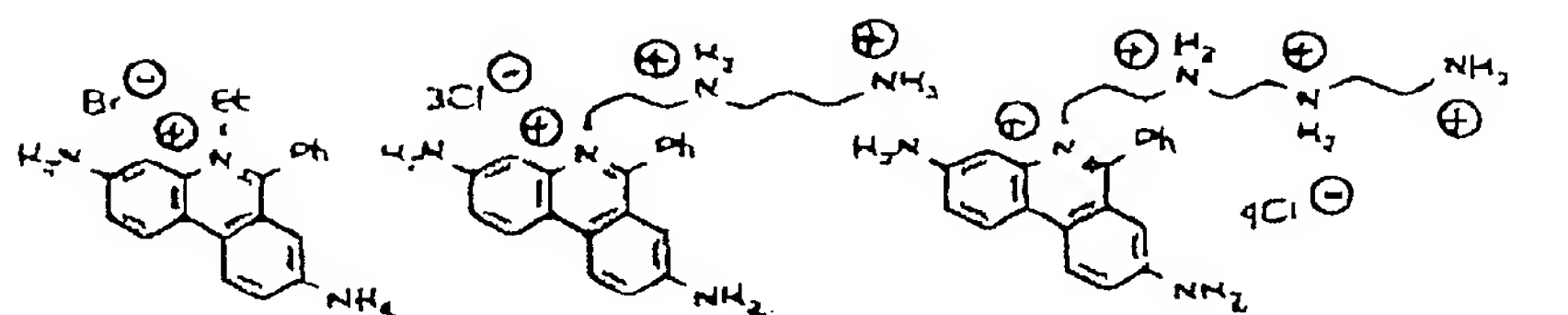
CAGGGTAC▼

5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

d

FIGURE 54

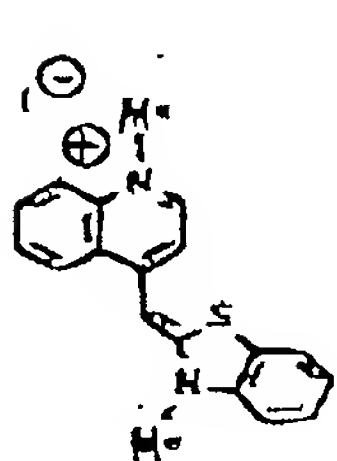
FIGURE 55



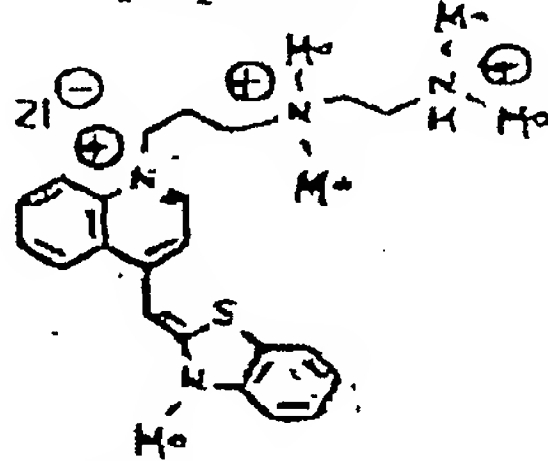
Ethidium Bromide

(1,3-propanediamino)-
propidium

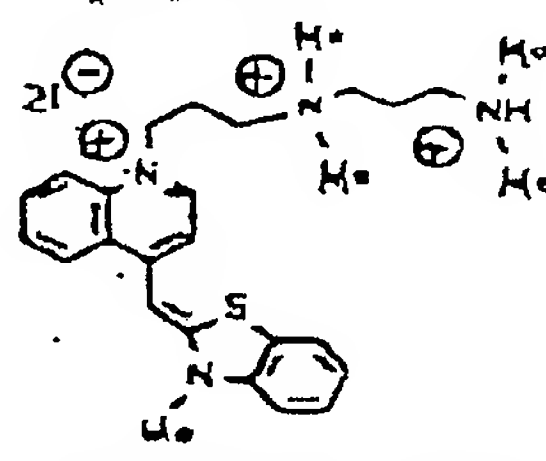
(diethylenetriamino)-
propidium



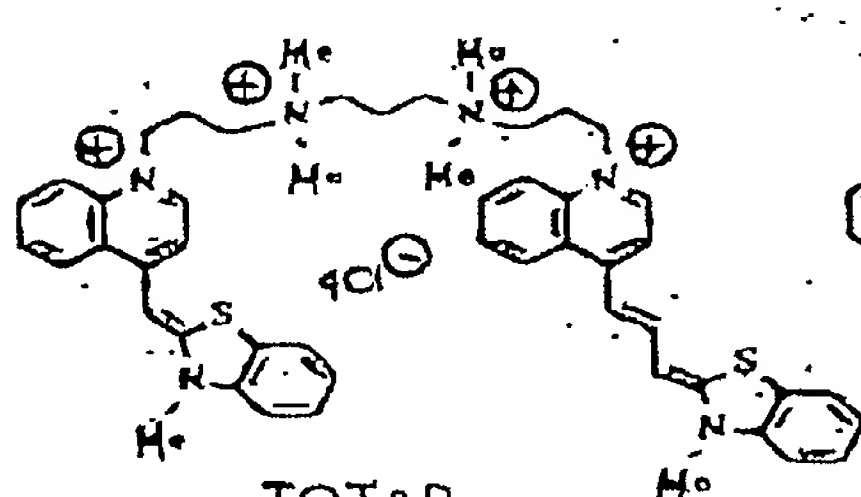
Thiazole Orange



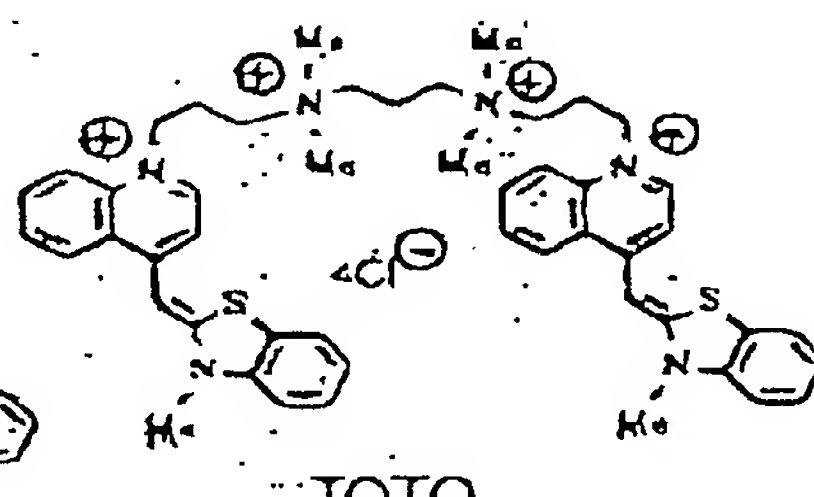
(N,N'-tetramethyl-
1,2-ethanediamino)-
propyl thiazole orange



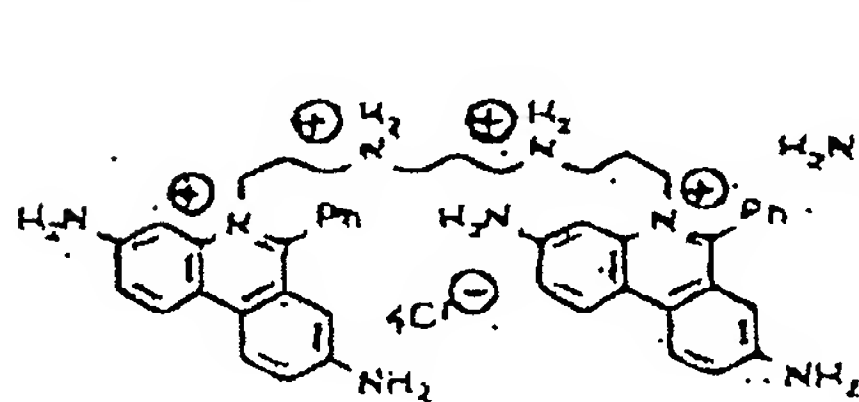
(N,N'-tetramethyl-1,3-propanediamino)-
propyl thiazole orange



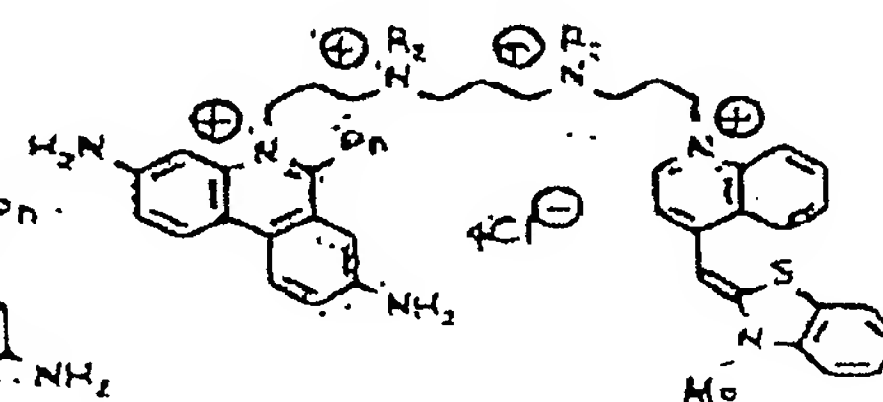
TOTAB



TOTO



EtHO

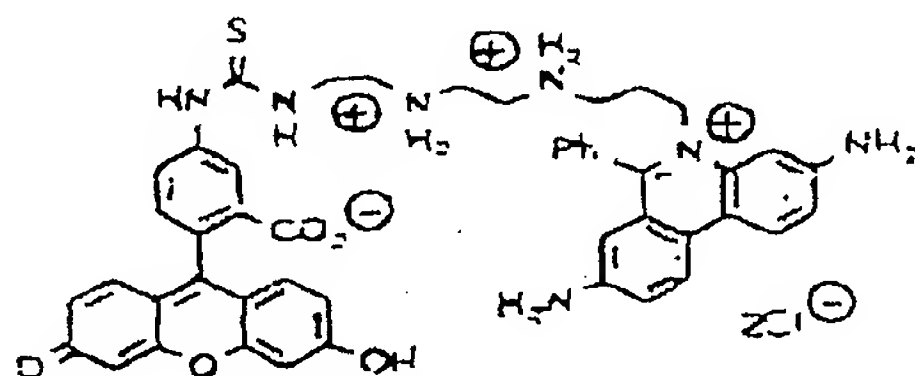


TOED1

(R = H)

TOED2

(R = CH₃)



FED

FIGURE 56

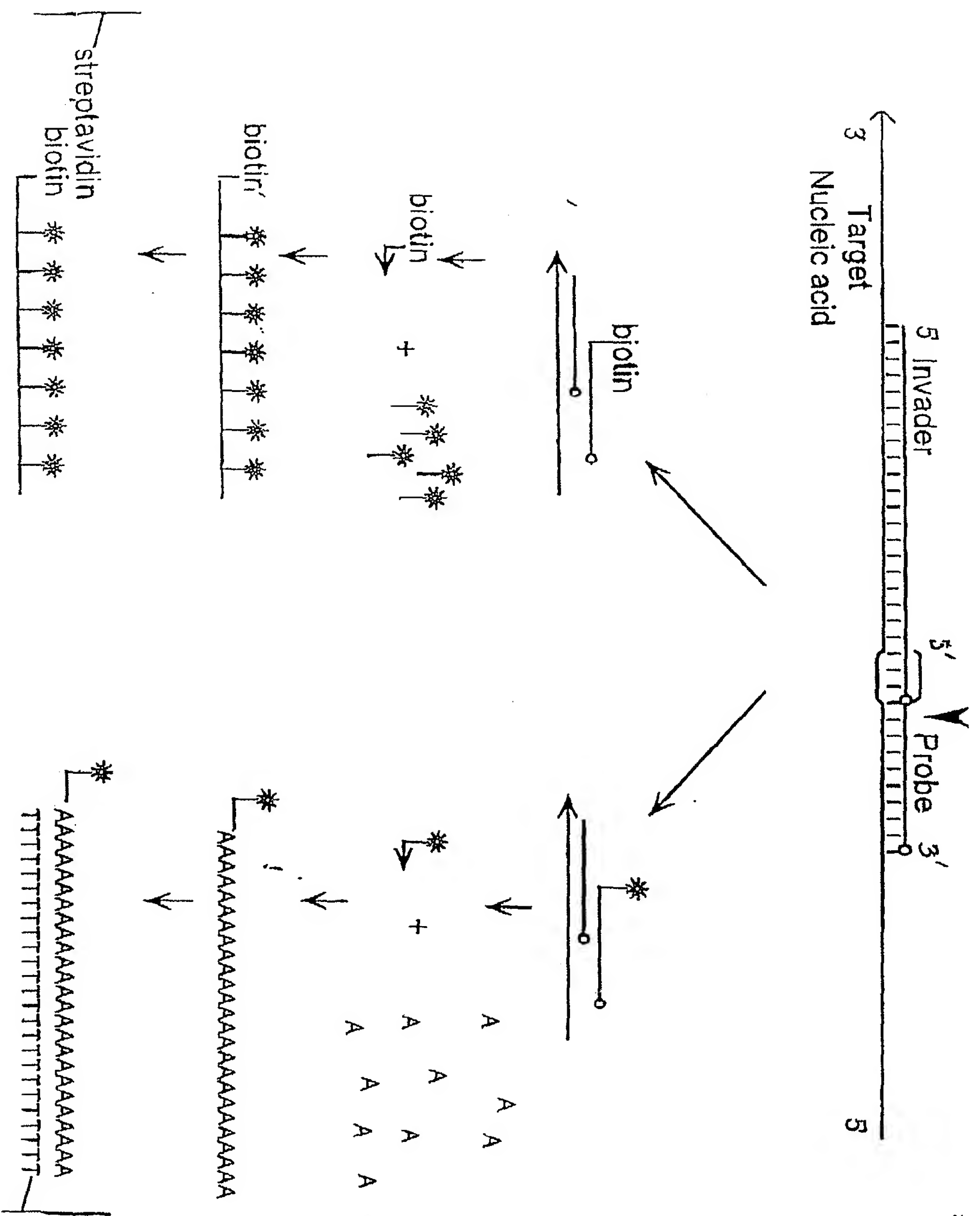


FIGURE 57

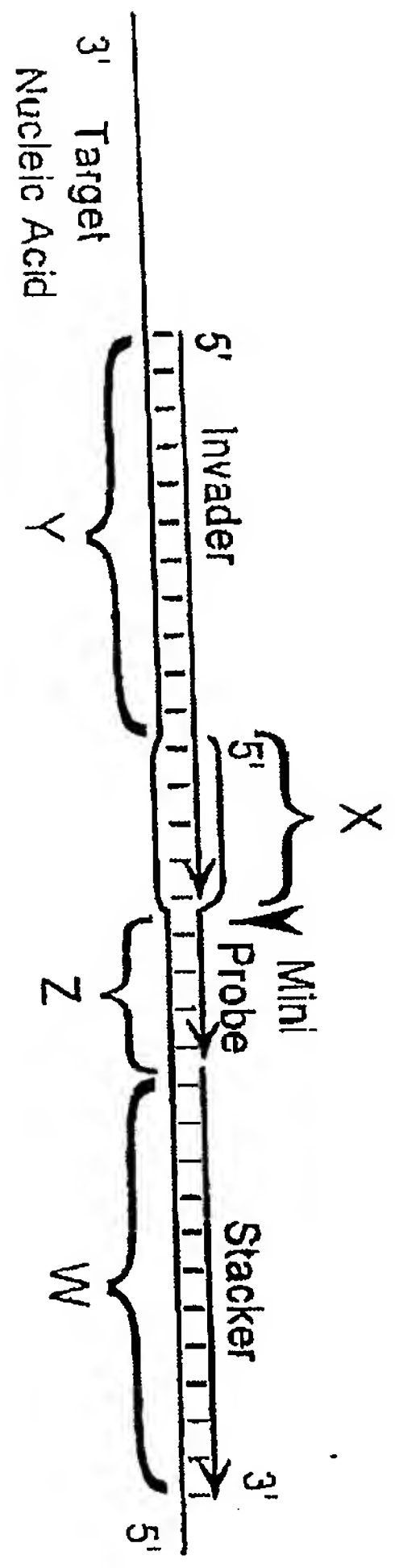


FIGURE 58



71

[illegible]

72

CELRAD2.PRO

CELRA02.PRO

FIGURE 59C

	290	300	310	320	330	340	350	
1	EEVDEIKRIFKEPKV-----			TD--NYSLSKLPDKEGIIKFLVDENDFN			YD	MJAFEN1.PRO
2	SDYDLIAIKEFFLNPPV-----			TO--NYNLVWRDPDEEGILKFLCDEHOF			SEE	PFUFEN1.PRO
3	ENWELHKEAHOLFLEPEV-----			LOPESVELKWSEPNEEELIKFMCGEKOF			SEE	HUMFEN1.PRO
4	ENWELHKEADOLFLEPEV-----			VOPESVELKWSEPNEEELVKFMCGEKOF			SEE	MUSFEN1.PRO
5	EEDWPKRGARMLFLOPEV-----			IDGNEINLKWSPKKEKELIEYLCDDKKF			SEE	YST510.PRO
6	ETENKFEKDLRKKLYNNEI	ILDODFP	SVMYDAYMRPEVD	HDTPTFWGVP	PDLOMLRSFMKTOLGWPHE			YSTRAD2.PRO
7	EDVNTPVKKRINKLVGK-I	ILPSEFP	NPLVDEAYLHP	PAVDDSKOSFOWGIP	DLOELROFLMATVGWSKO			SPORAD13.PRO
8	EDNPHDTKVKKKL--	RTLQ	LTGFPNP	AVAEAYLKPV	VDDSKGSFLWGKPDLOKIREFCORYFGWNRT			HUMXPG.PRO
9	EDMPYDTKVKKKL--	RKLO	LTGFPNP	AVADAYLRP	VDDSRGSFLWGKPDVDKIREFCORYFGWNRM			MUSXPG.PRO
10	EDAPNDTKVKKKL--	RLLO	DOSFPNP	AVASAYLKPV	DESKSAFSWGRPDLEOIREFCESRFGWYRL			XENXPG.PRO
11	-----	EKKVSRPHL	ISTAILLGCDYF	ORGVONIGIVSVFO-	ILGEFGDGNEEIOPHVILDRFASYVRE			CELRAD2.PRO
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FIGURE 59D

	430	440	450	460	470	480	490
1							MJAFEN1.PRO
2							PFUFEN1.PRO
3							HUMFEN1.PRO
4							MUSFEN1.PRO
5							YST510.PRO
6							YSTRAD2.PRO
7							SPORAD13.PRO
8							HUMXPG.PRO
9							MUSXPG.PRO
10							XENXPG.PRO
11							CELRAD2.PRO
12							
13							
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FIGURE 60

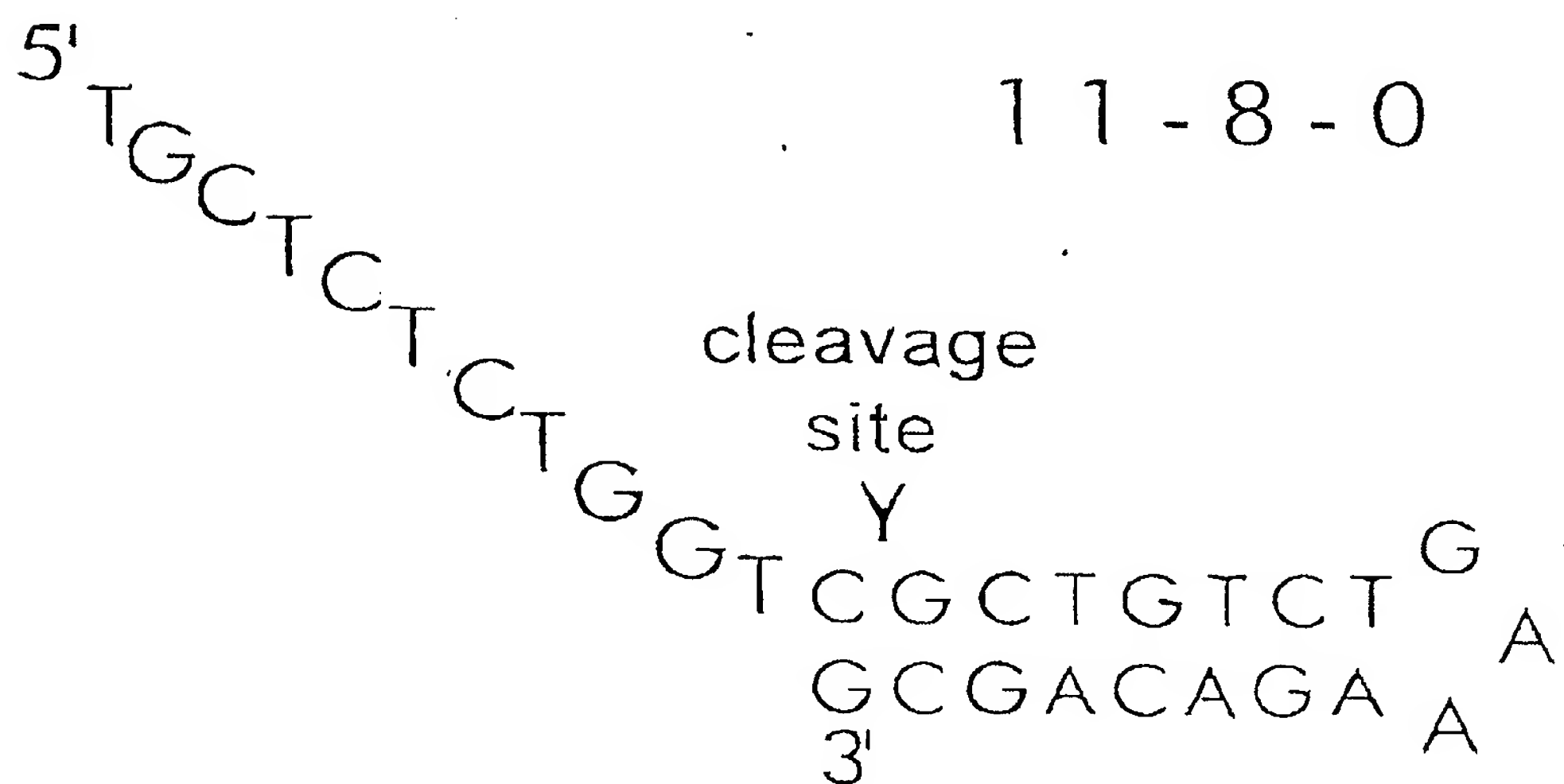
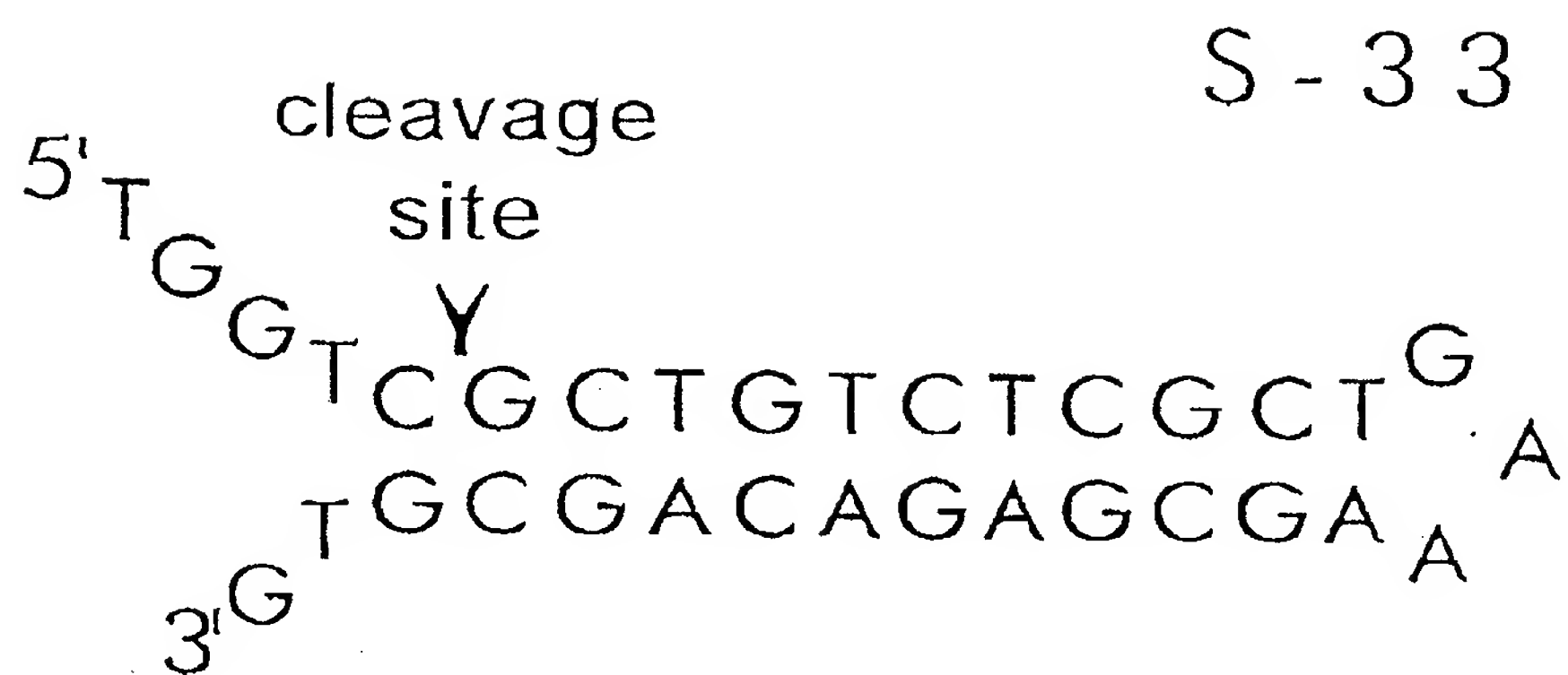


FIGURE 61

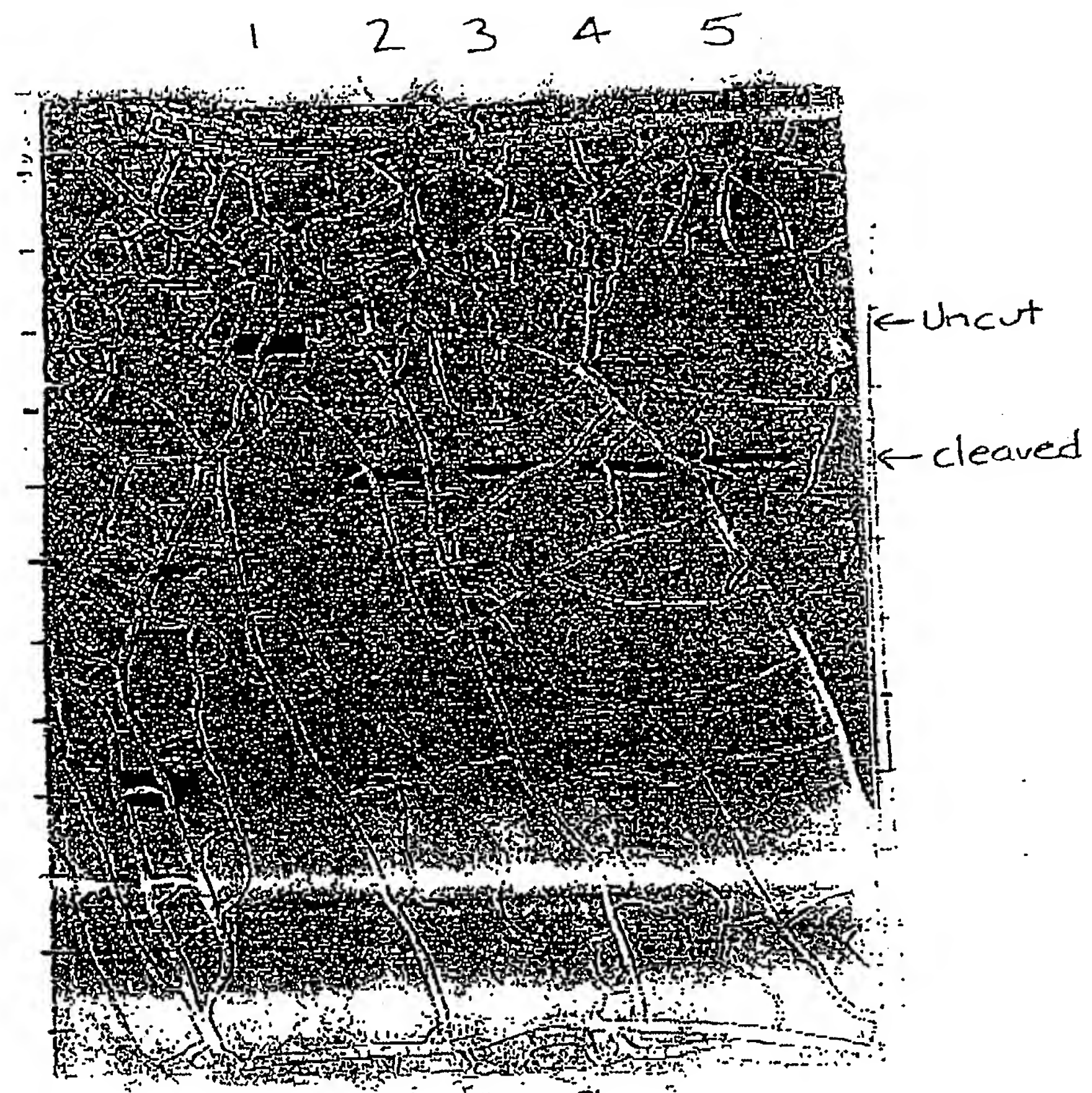


FIGURE 62

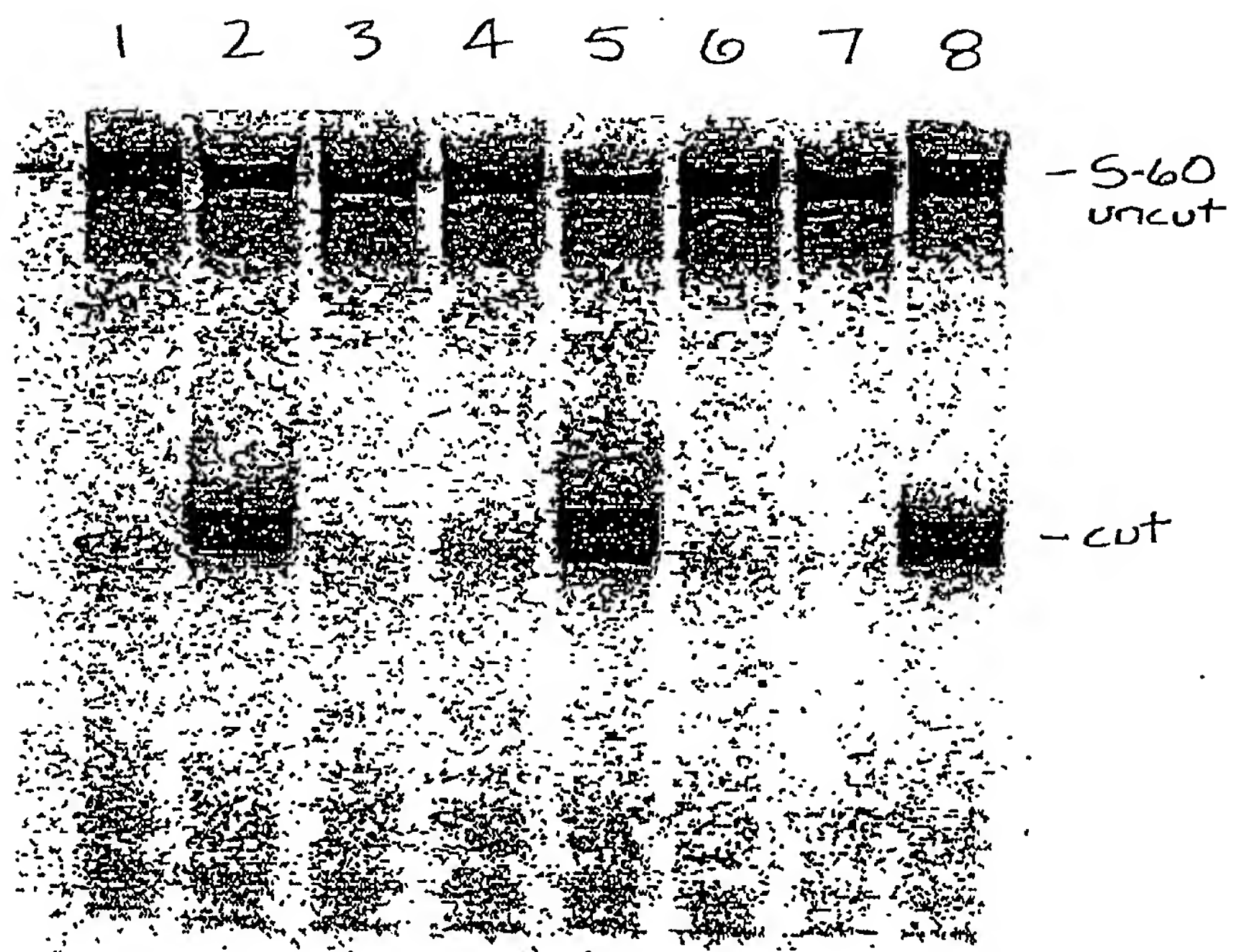
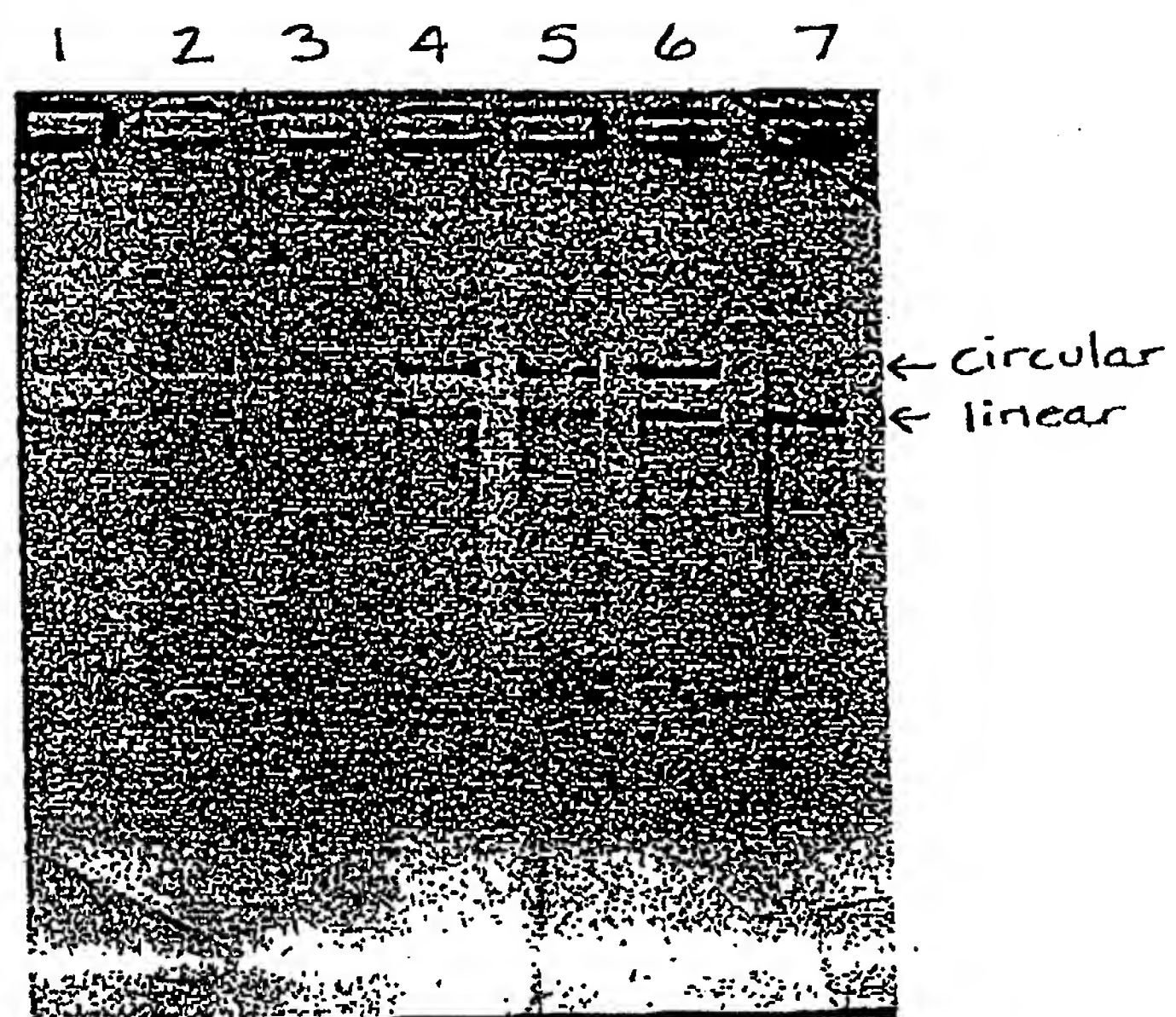


FIGURE 63



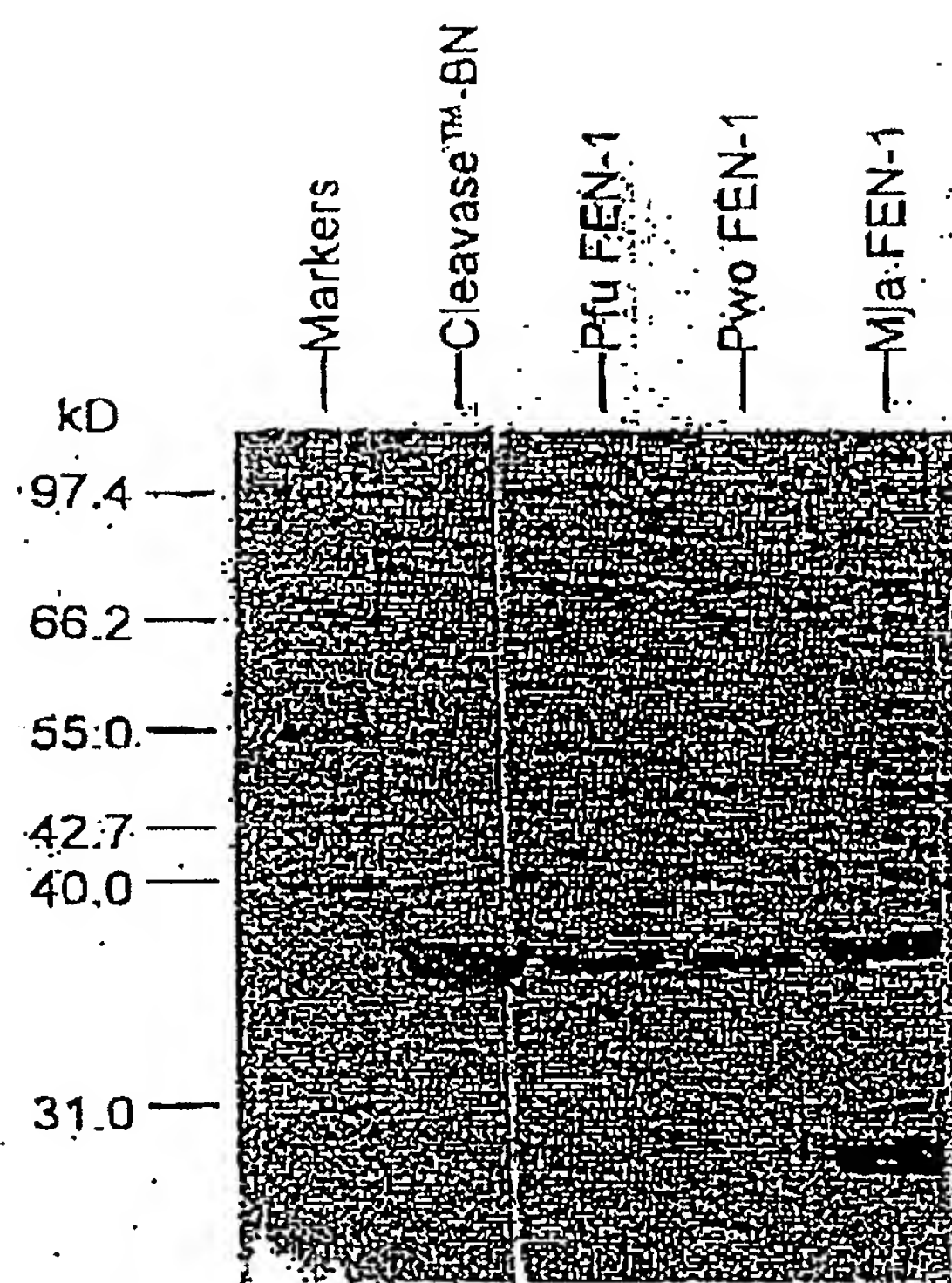


FIGURE 64

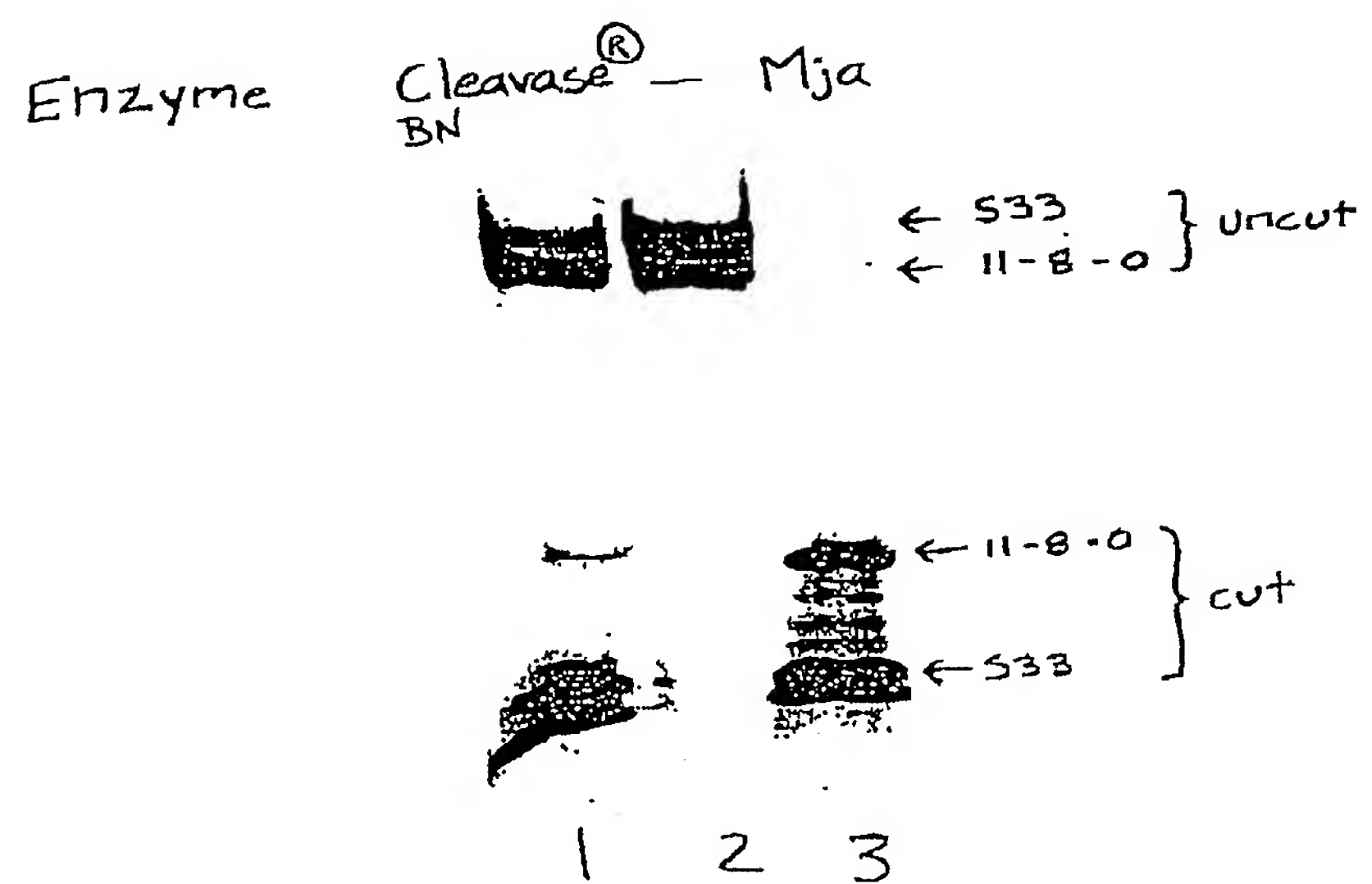


FIGURE 65

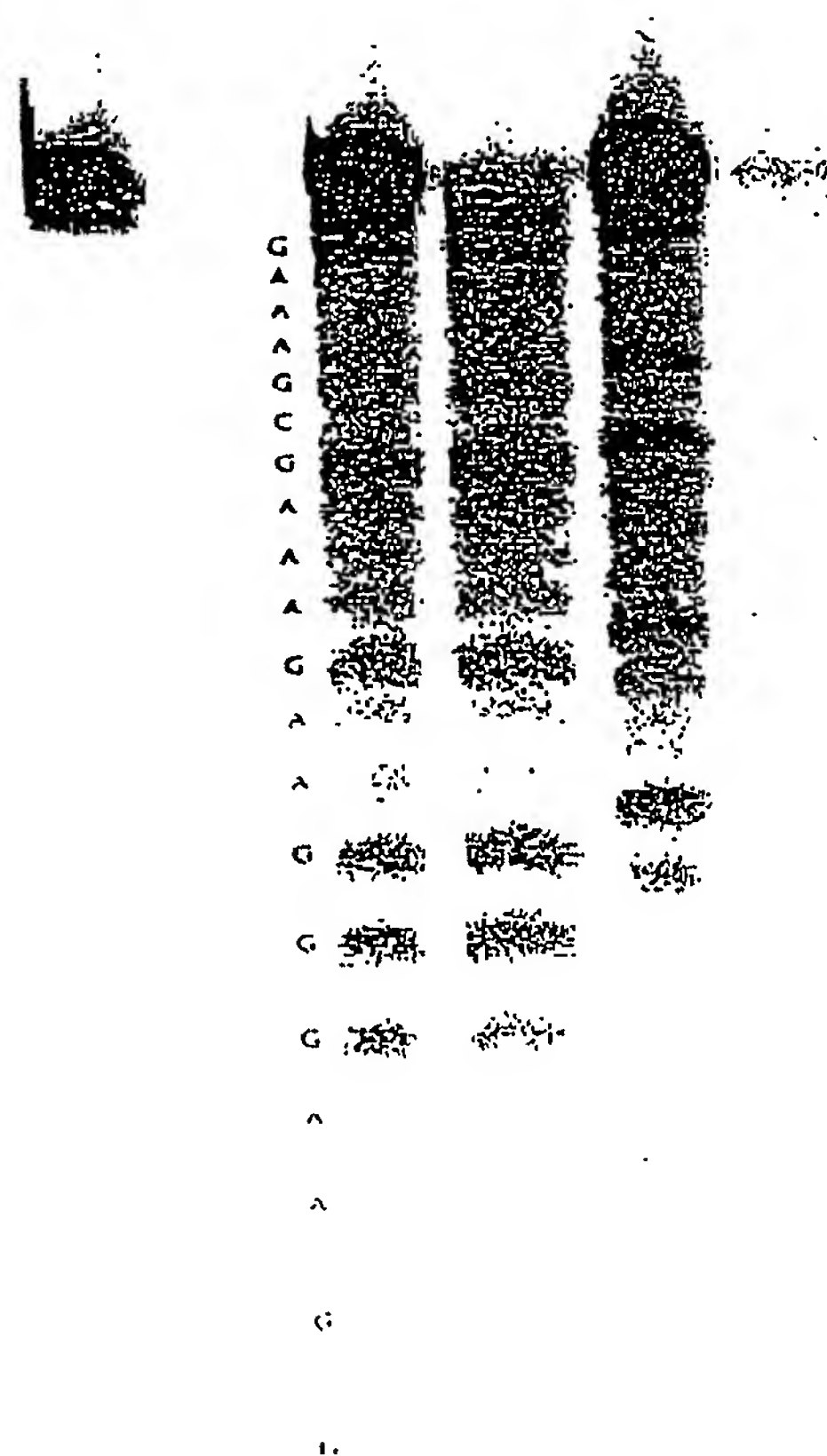
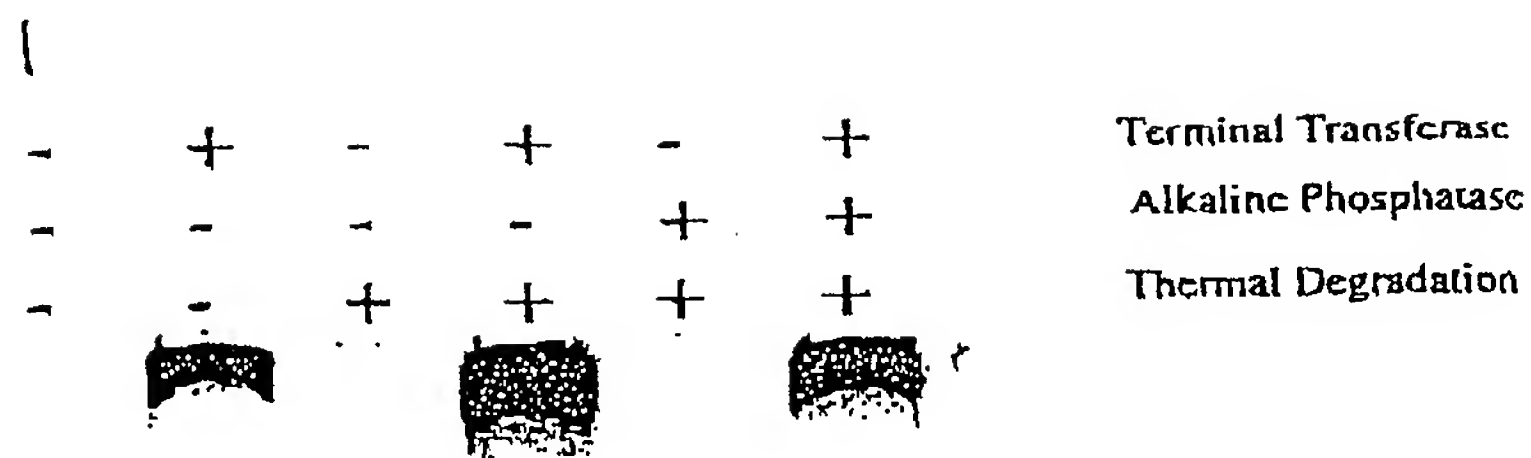


FIGURE 66

5'-nAGAAAggaagggga agaaagcgaaagG-3'

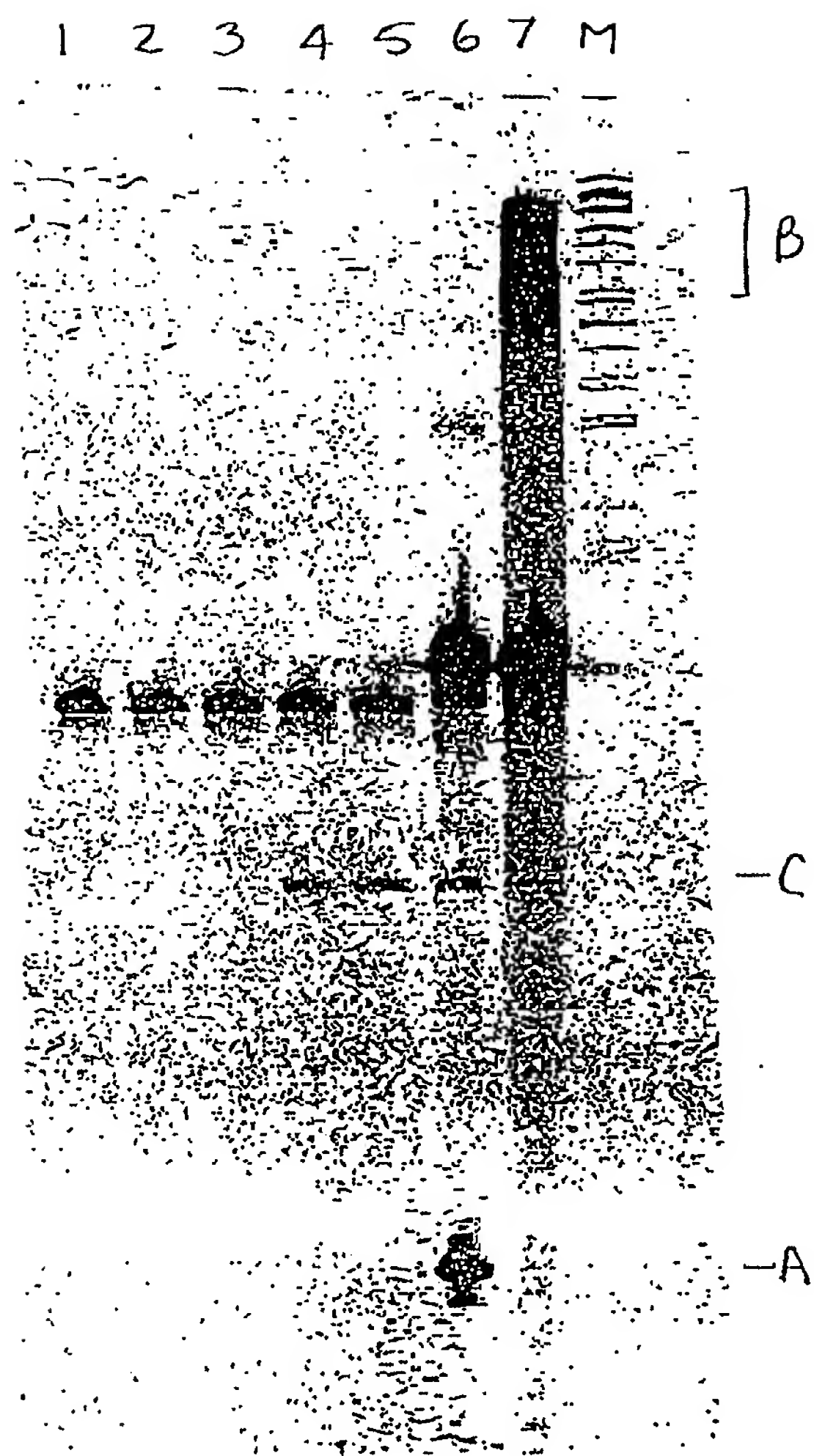


FIGURE 67

FIGURE 68

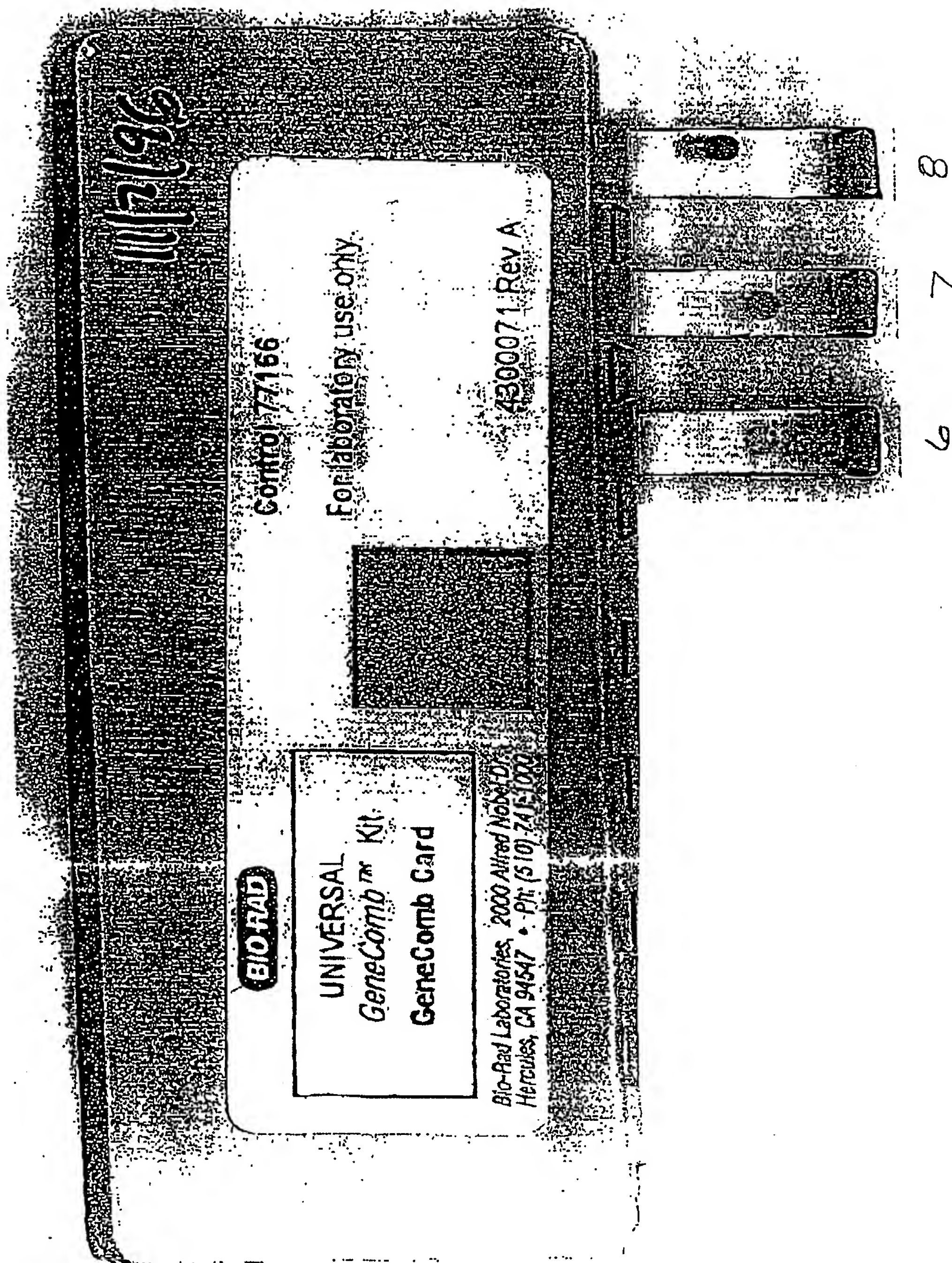


FIGURE 69

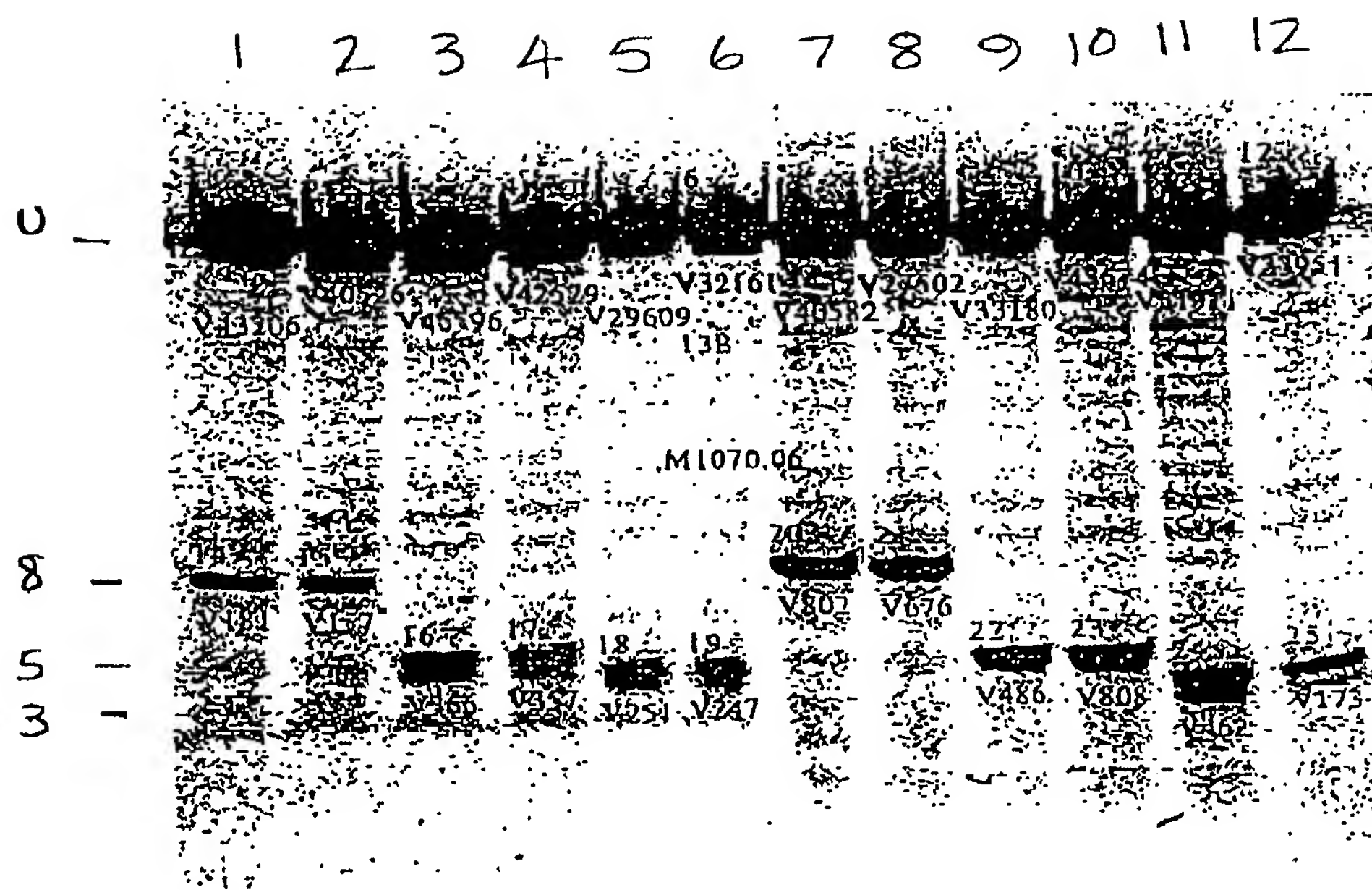


FIGURE 70

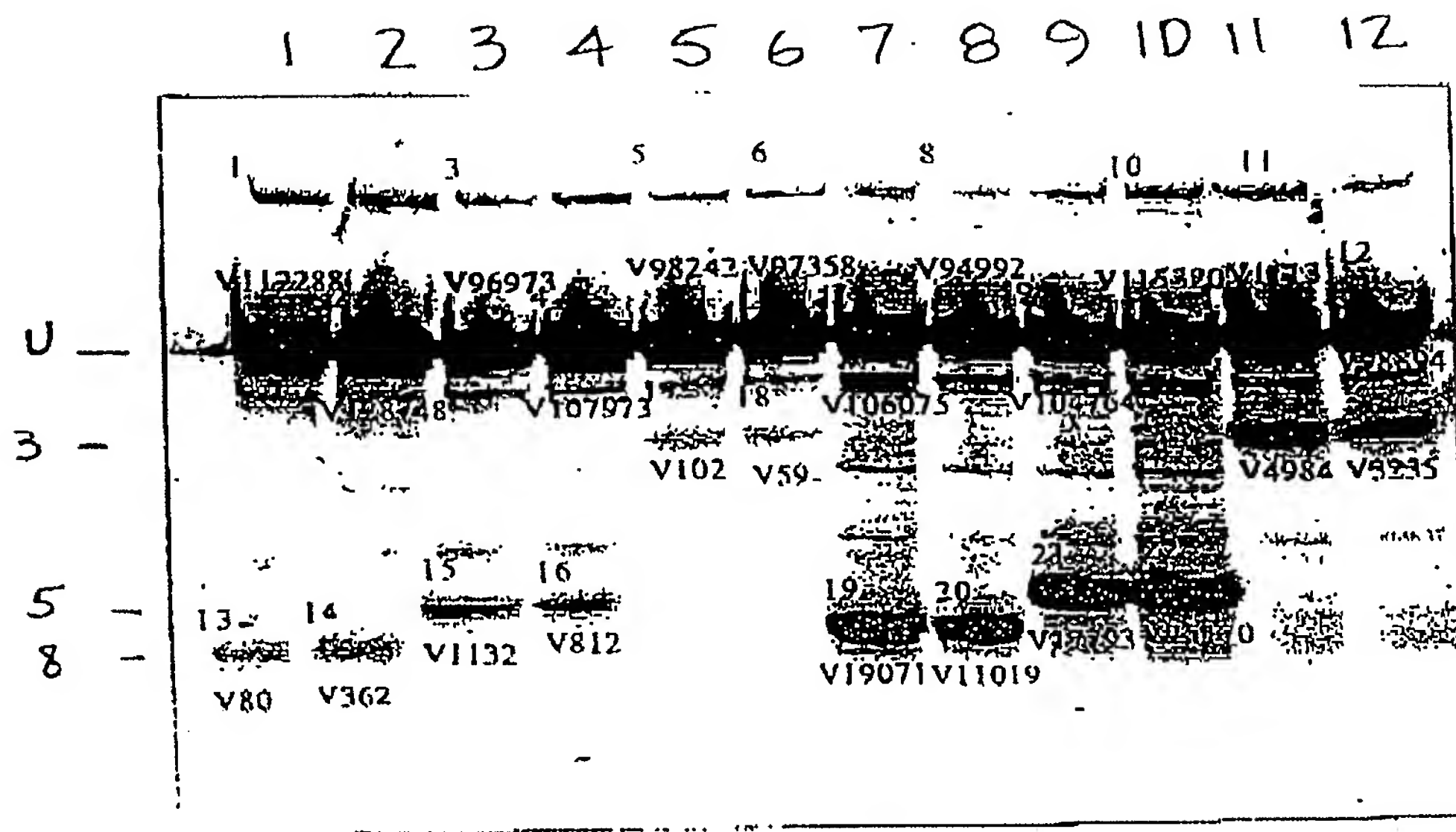
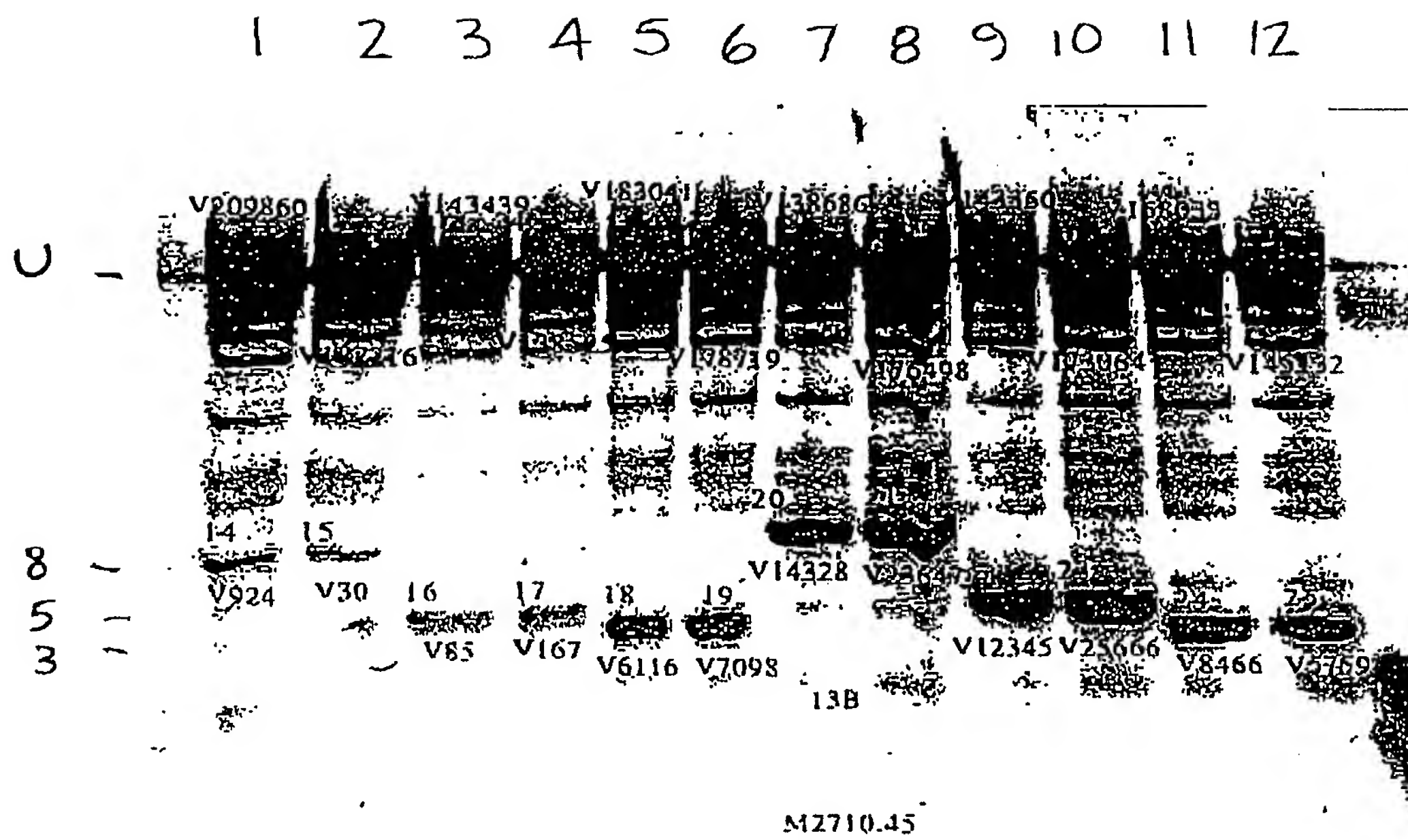


FIGURE 71



A

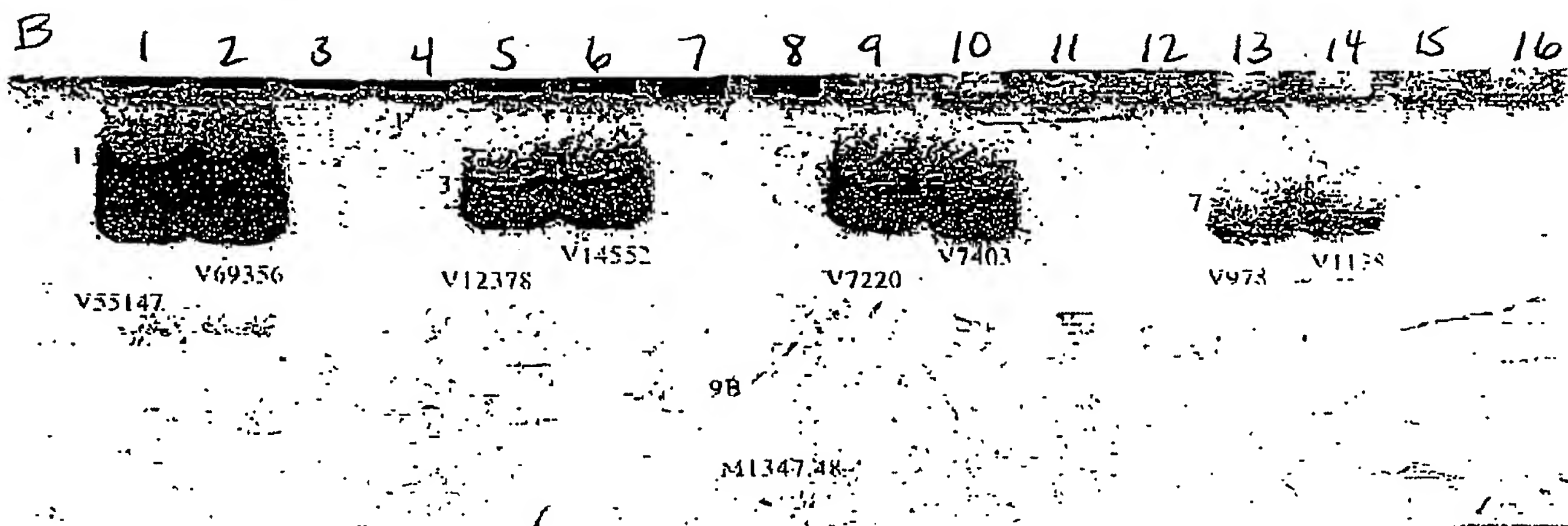
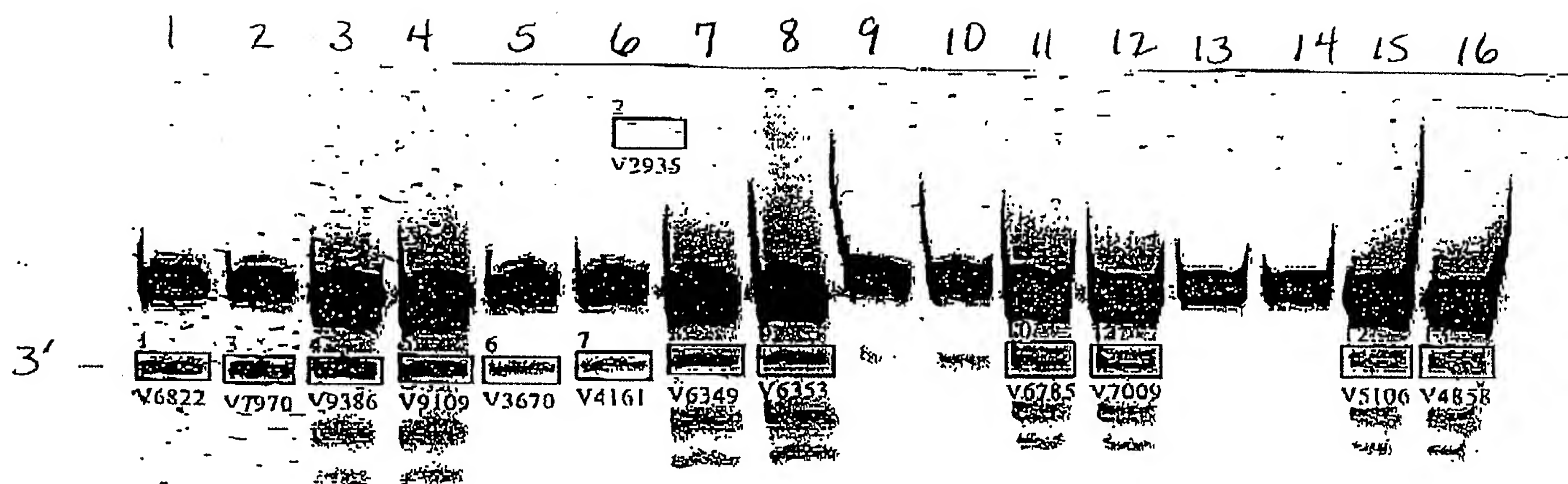
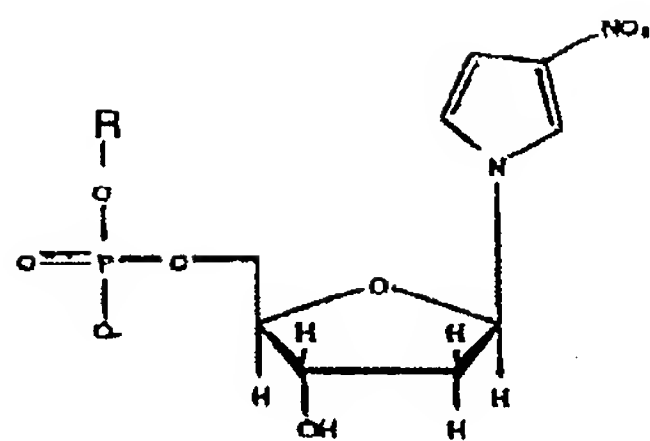
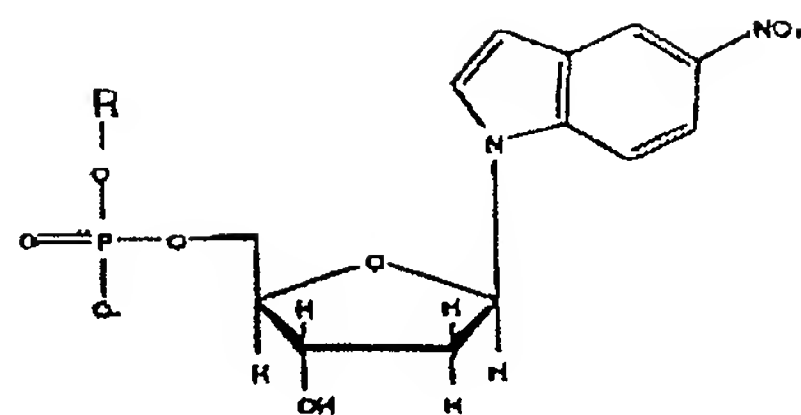


FIGURE 72

FIGURE 73



3-nitropyrrole



5-nitroindole

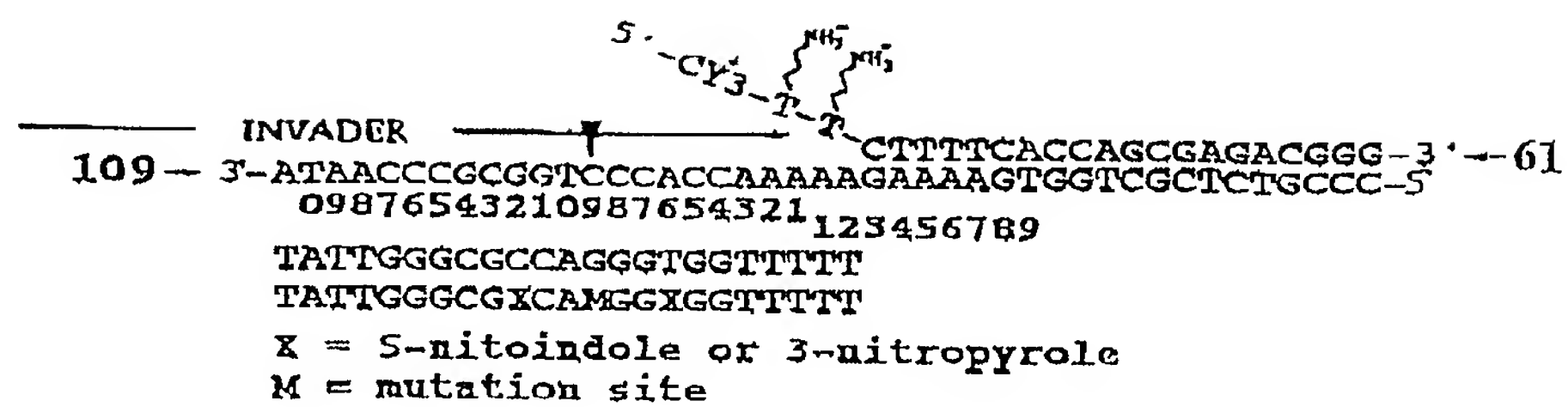
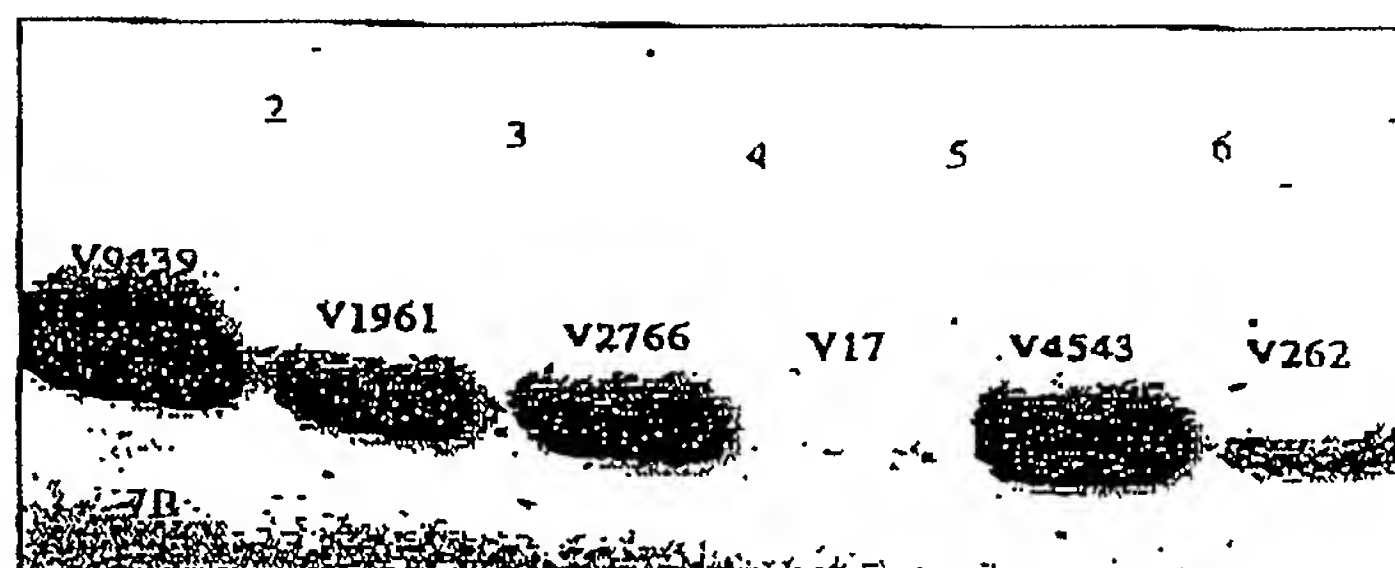


FIGURE 74

	All Comp	1 Base Mismatch	All Comp	1 Base Mismatch	All Comp	1 Base Mismatch
			2 NI	2 NI	1 NP	1 NP
Invert #	67	114	115	116	112	113

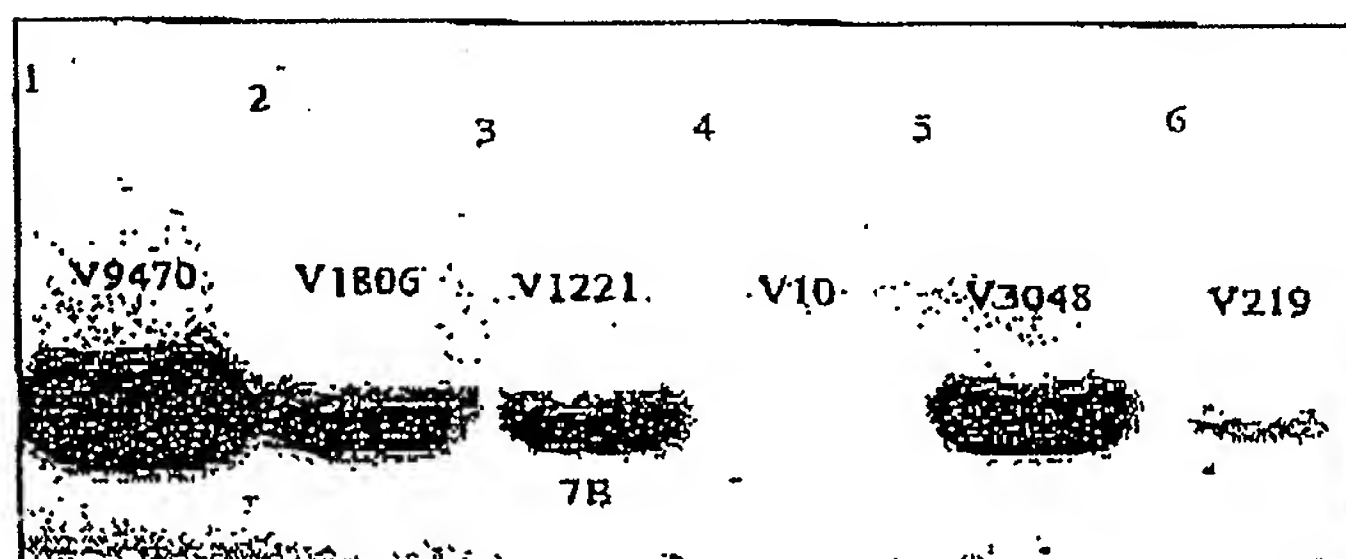
A

52°C



B

55°C



C

58°C

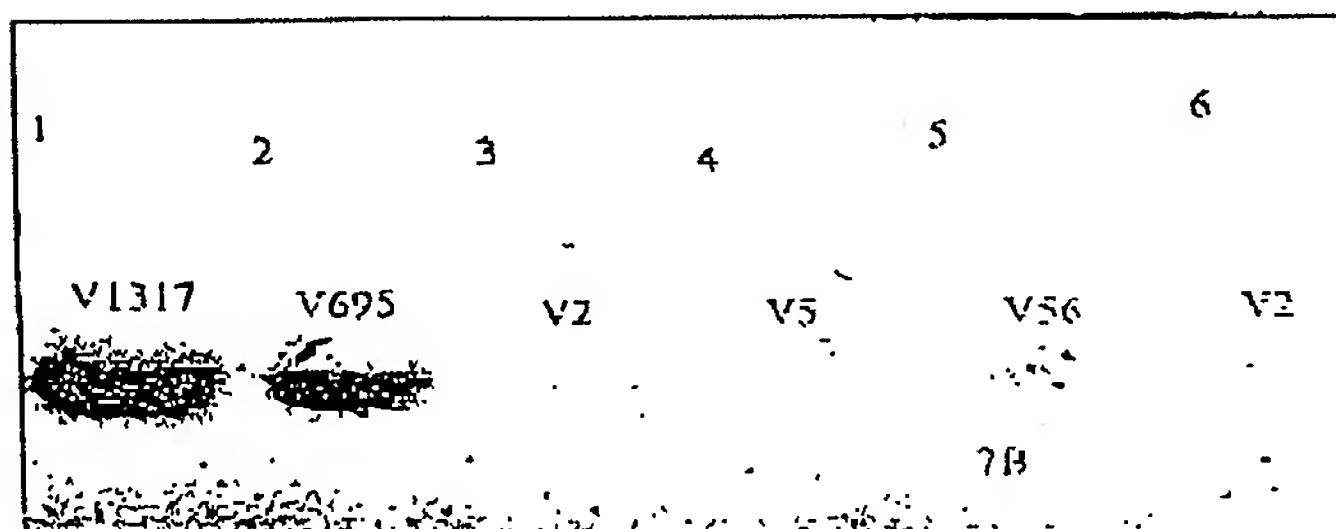


FIGURE 75

FIGURE 76

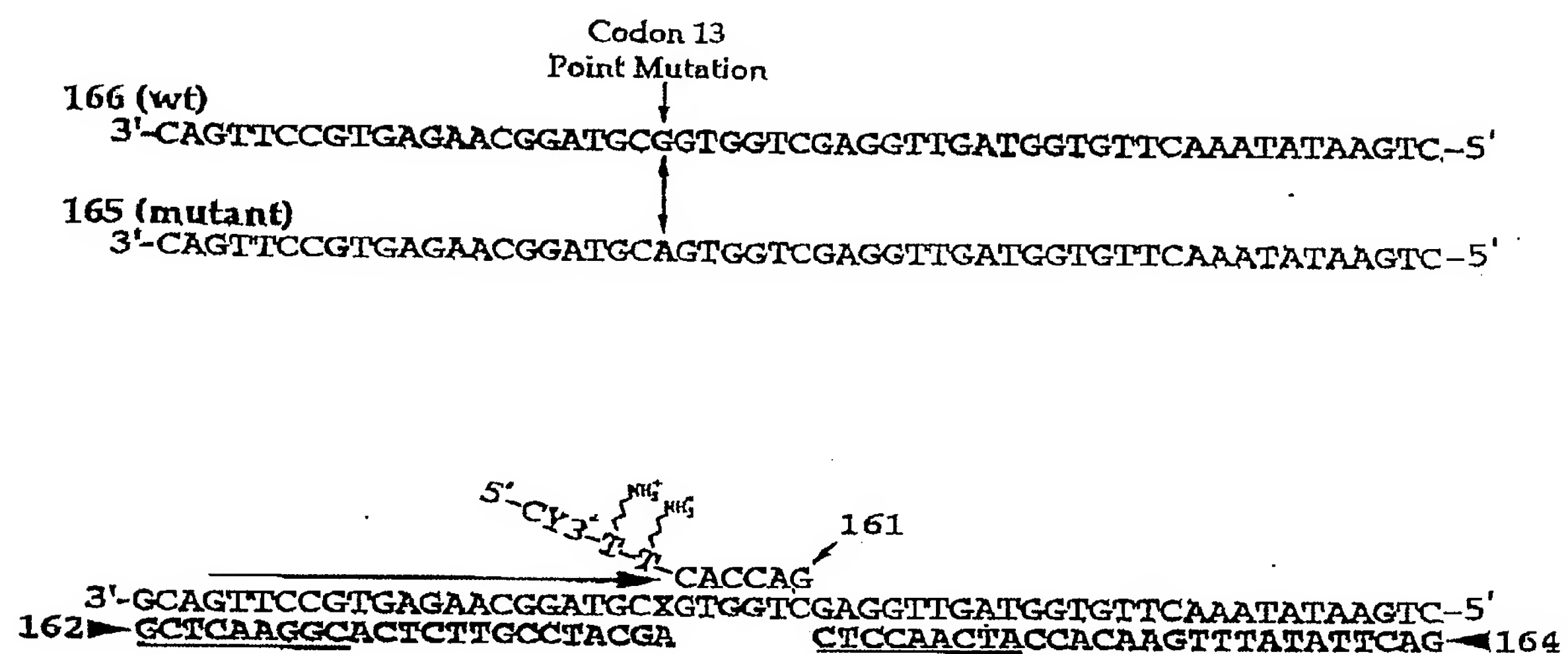


FIGURE 77

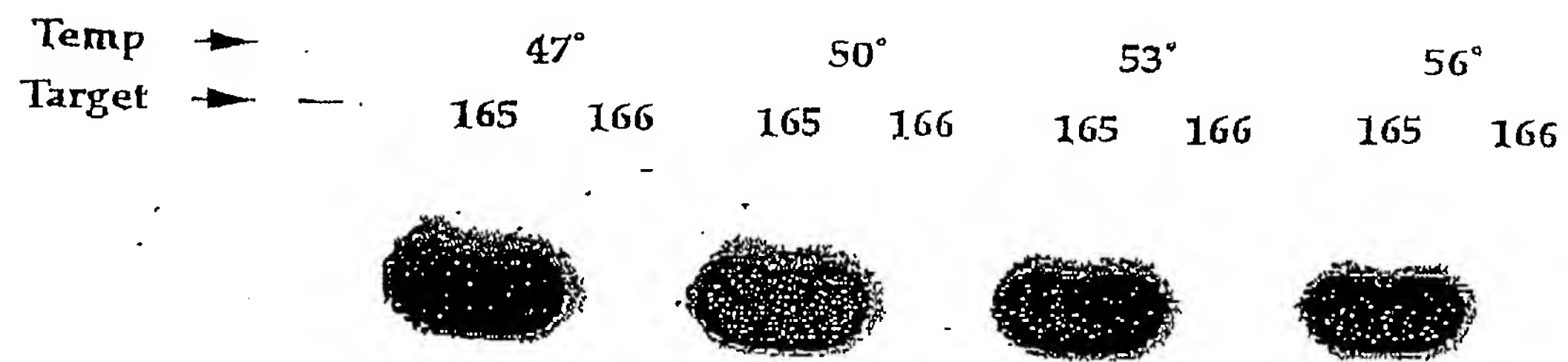
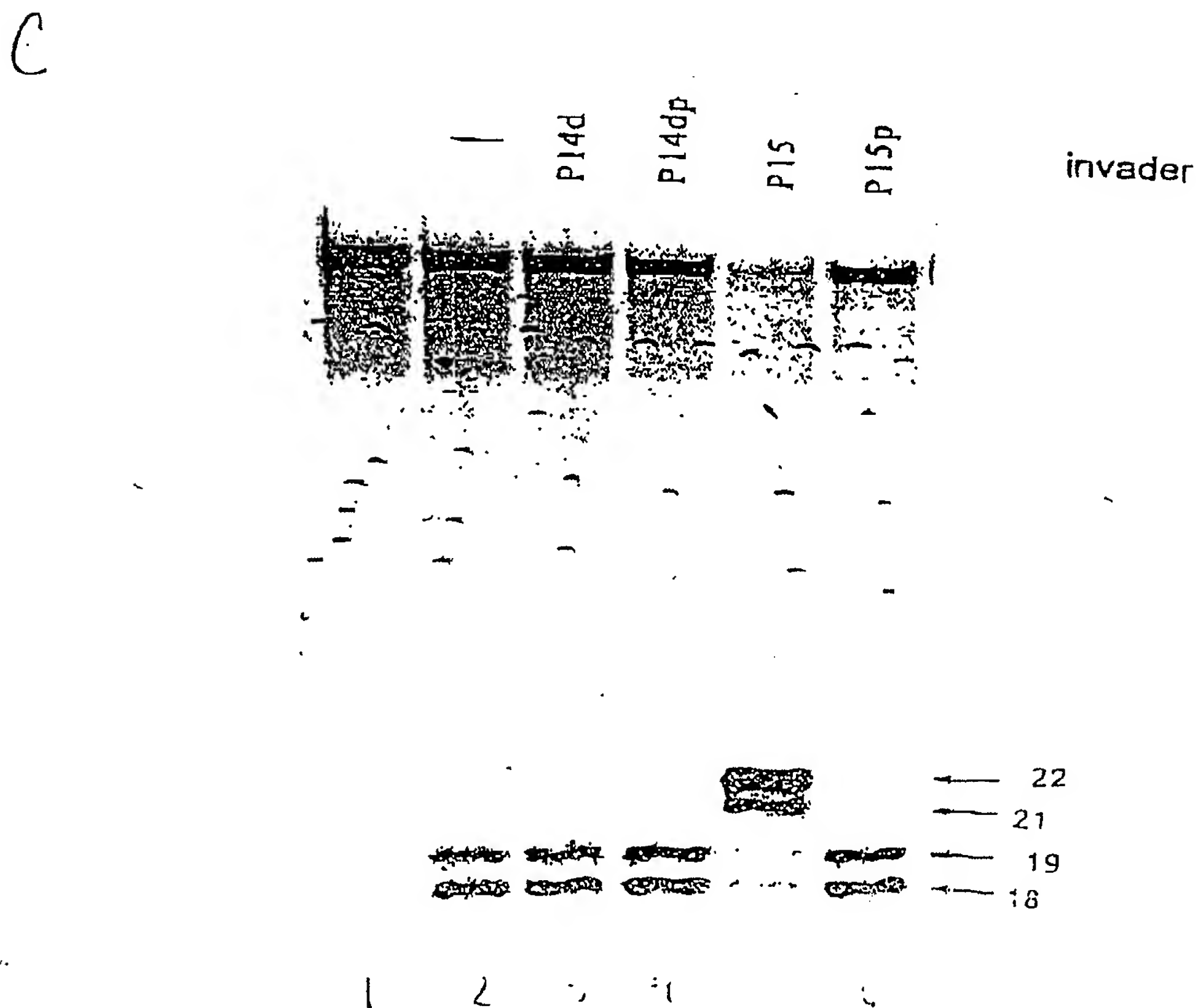
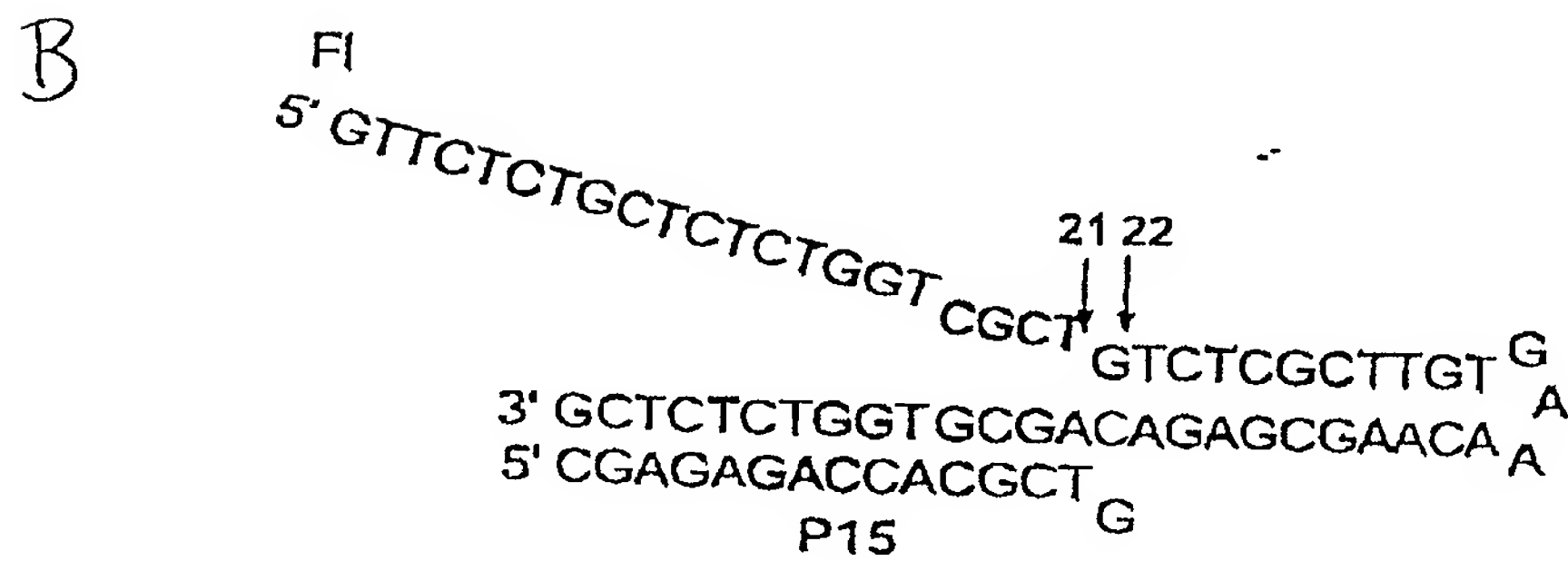
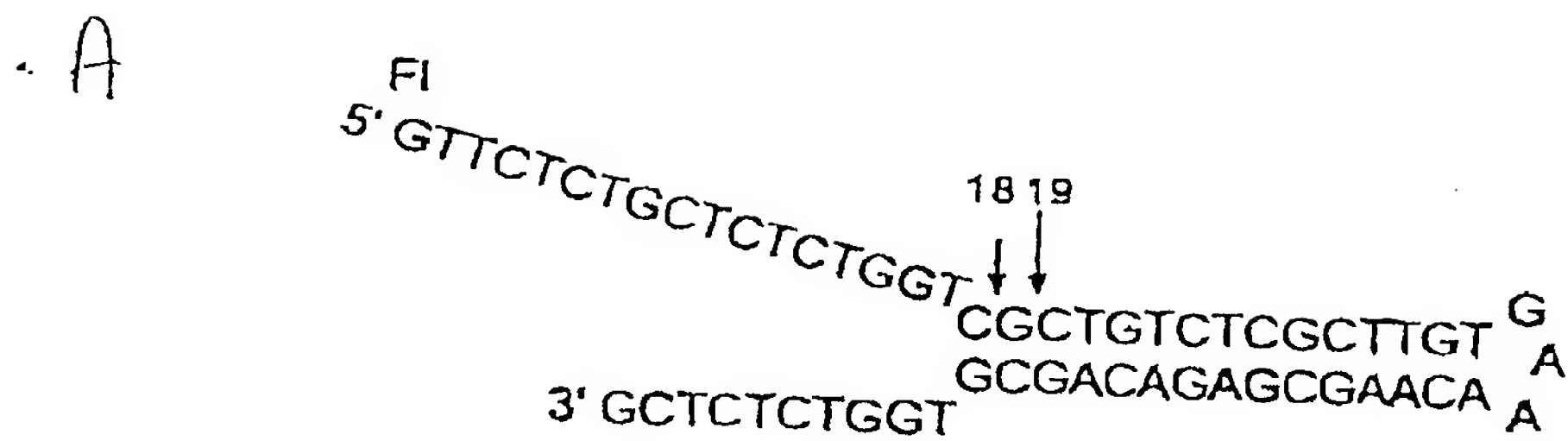


FIGURE 78



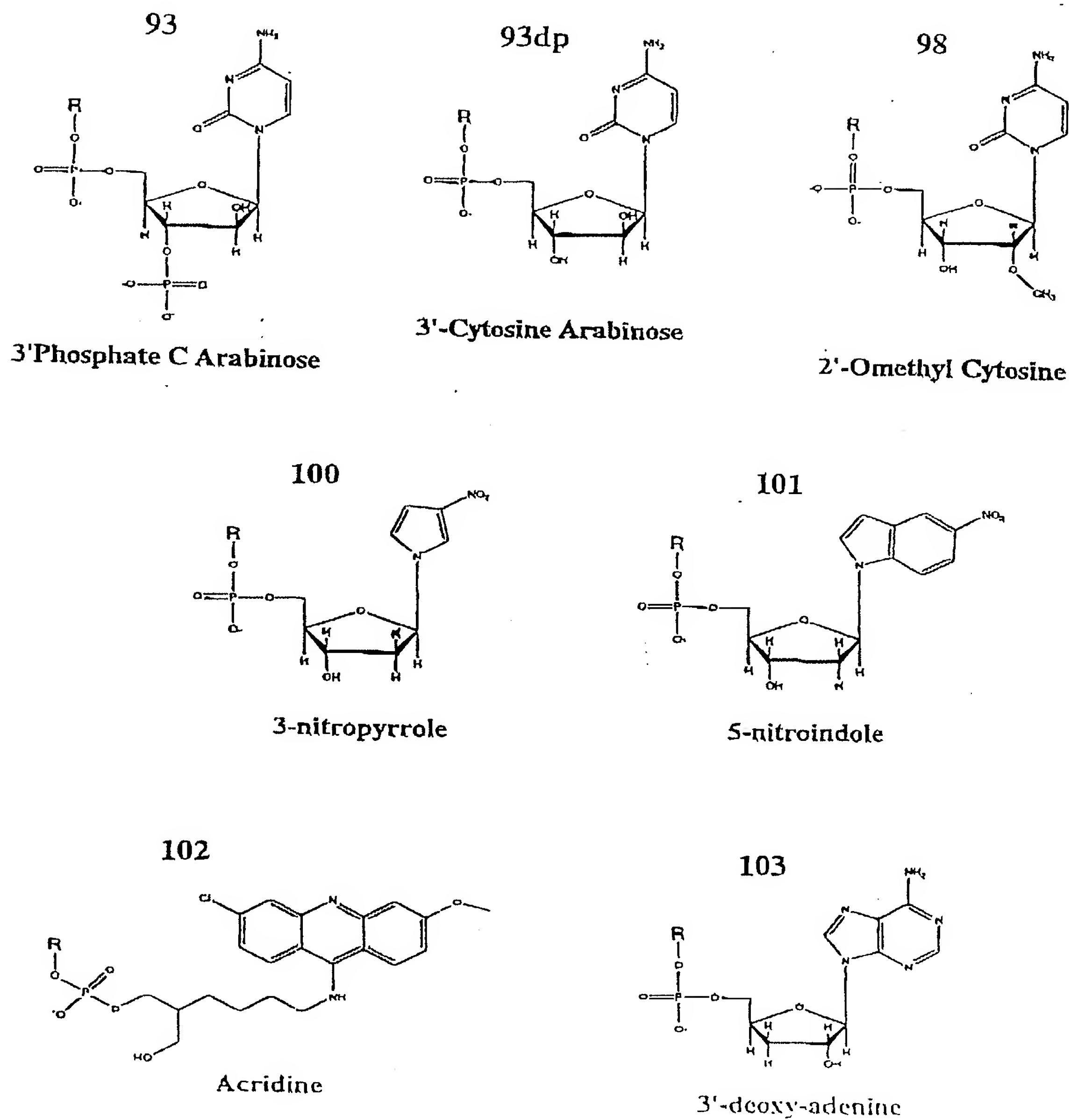


FIGURE 79

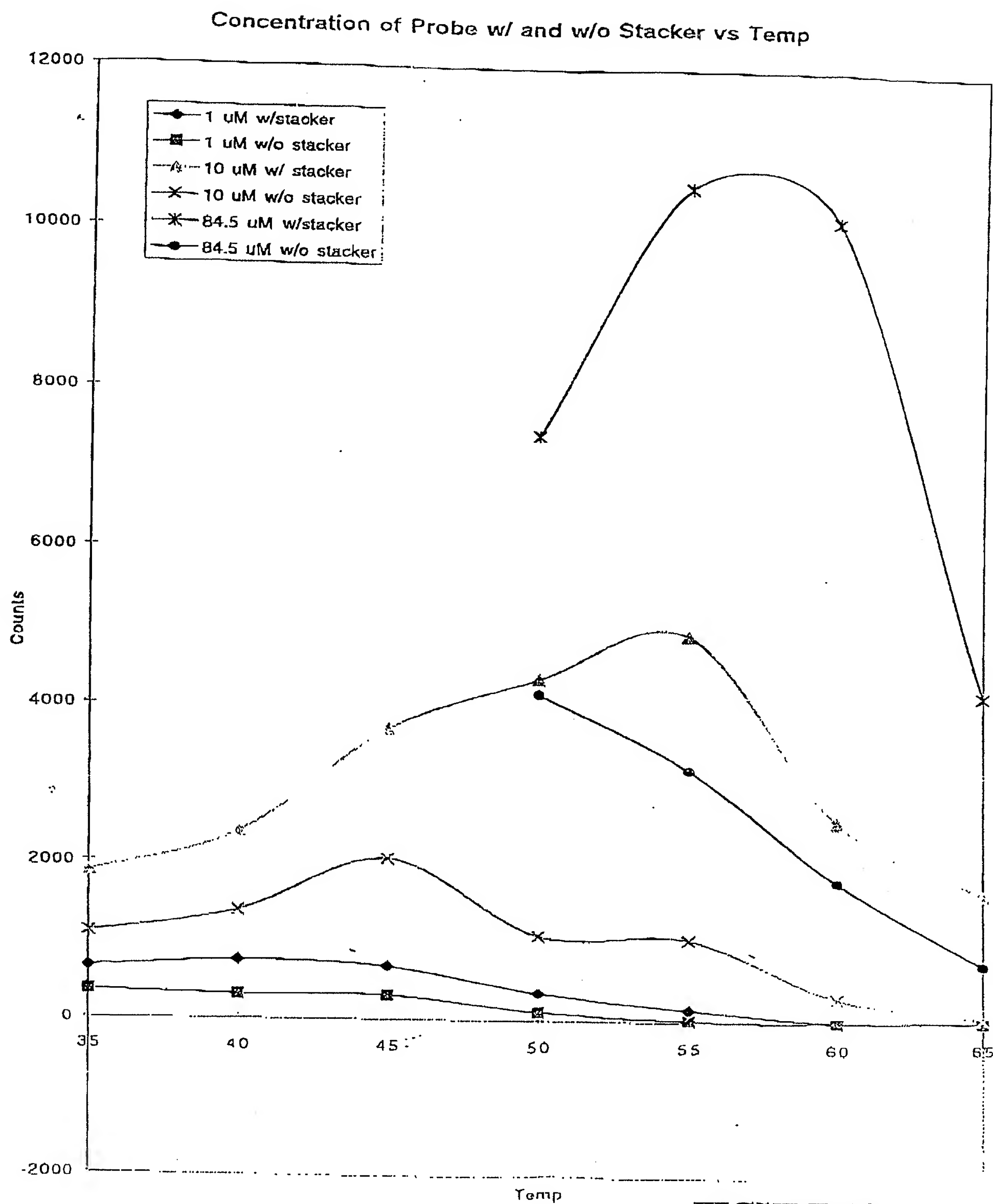


FIGURE 80

FIGURE 81

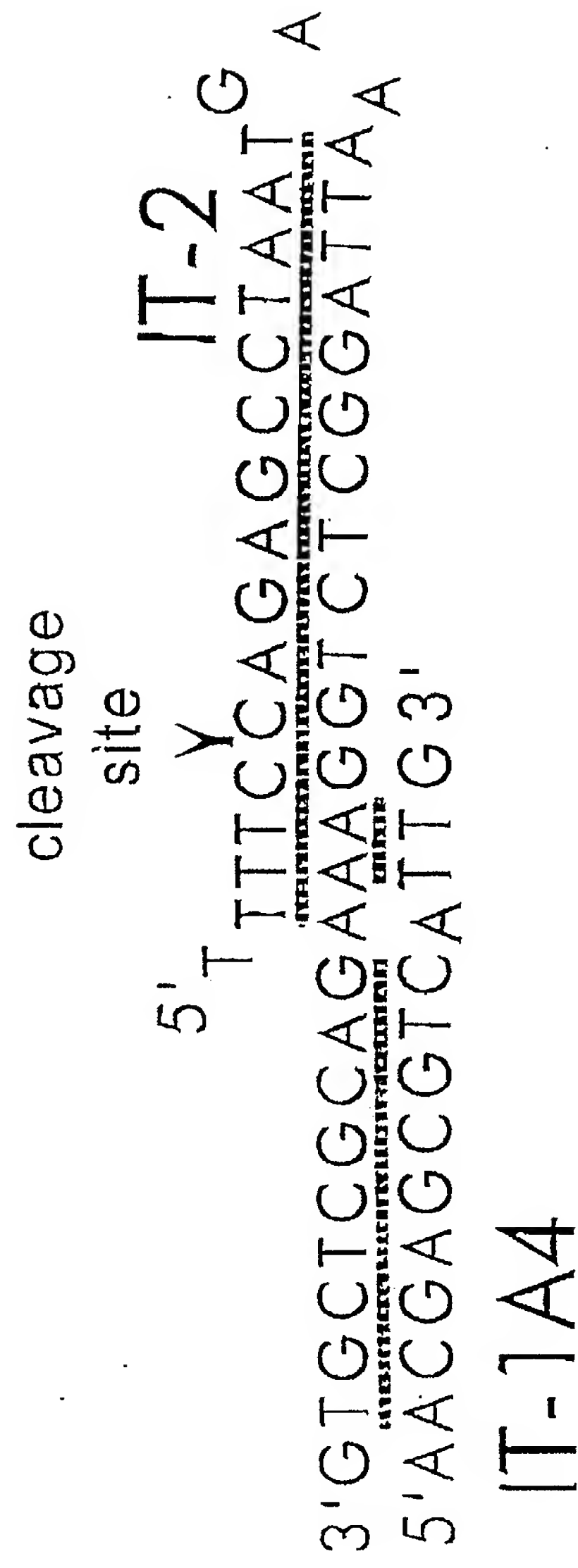
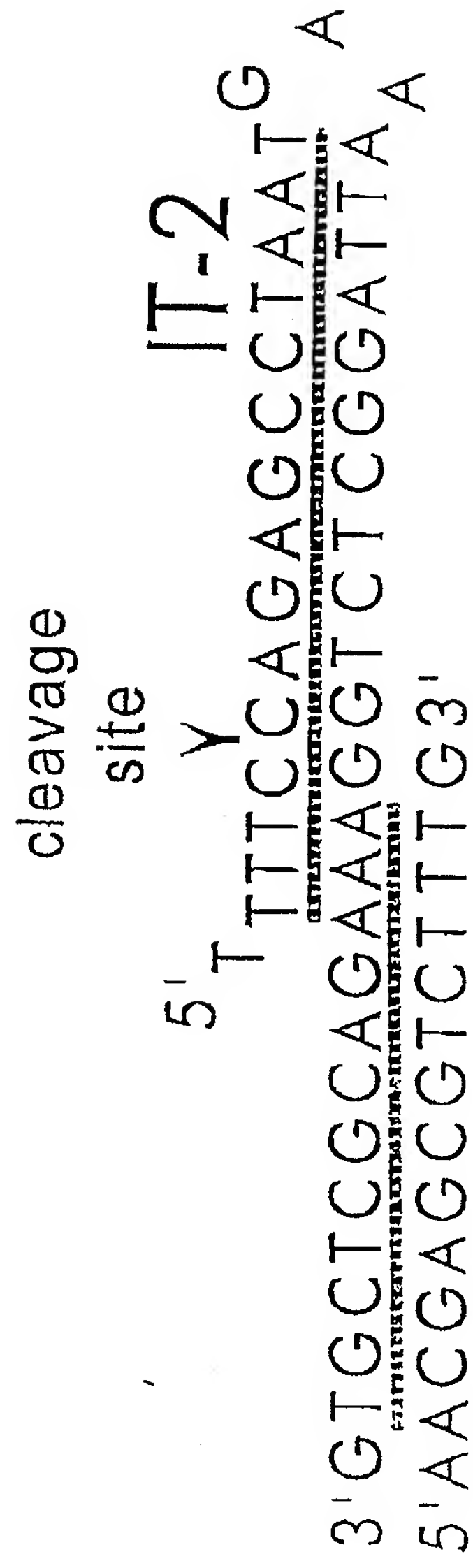


FIGURE 82

1 2 3 4



FIGURE 83

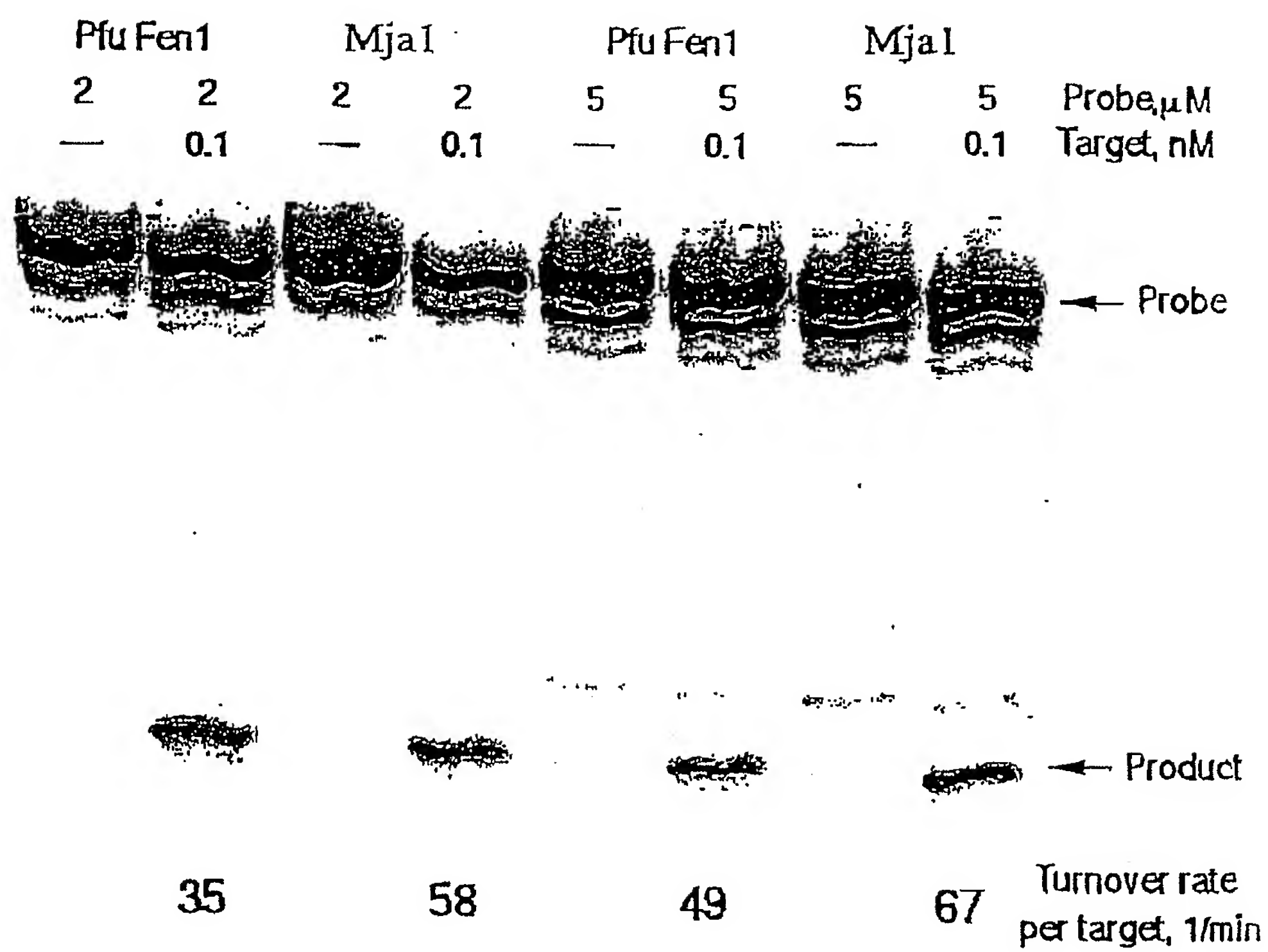


FIGURE 84

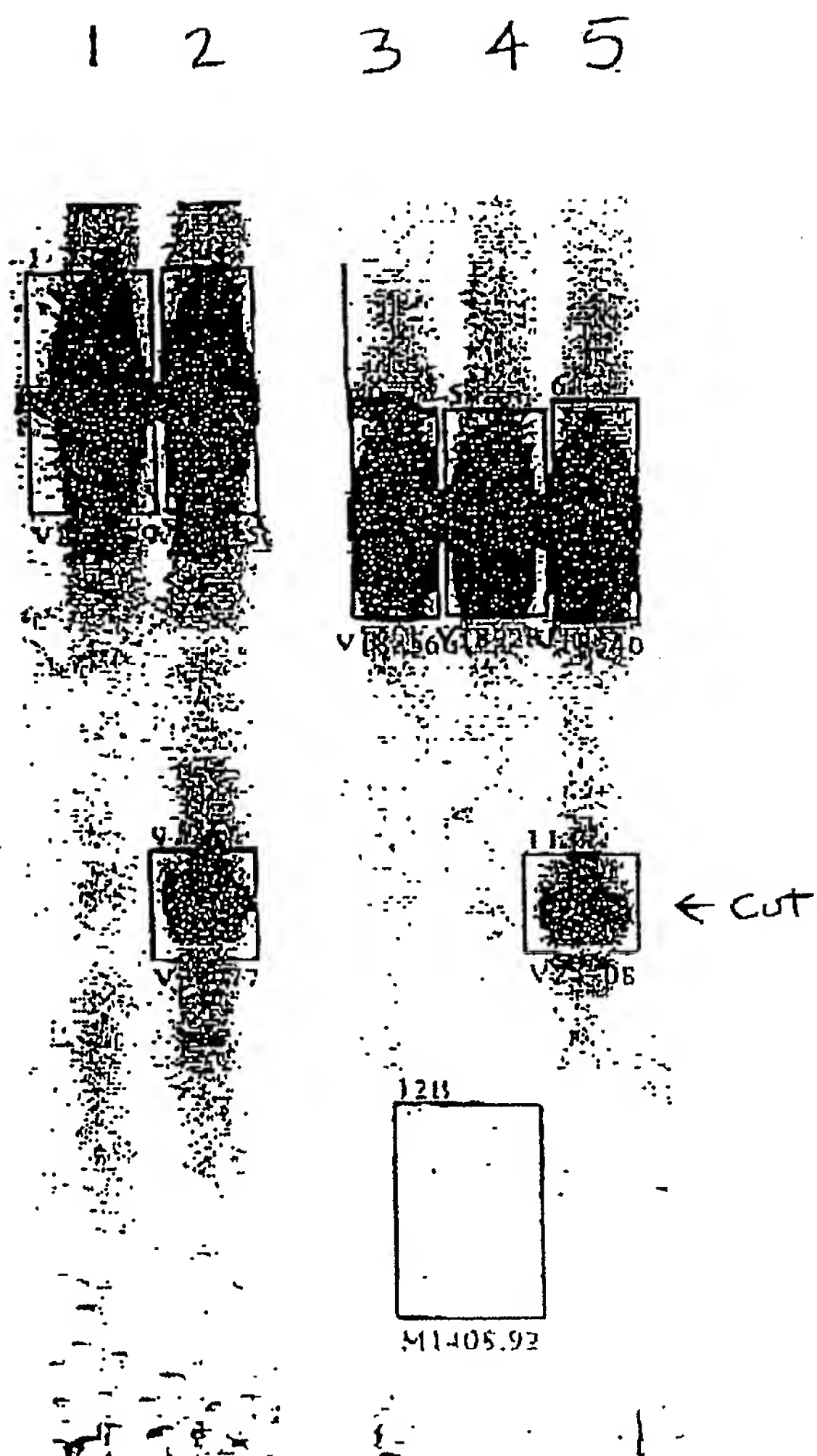
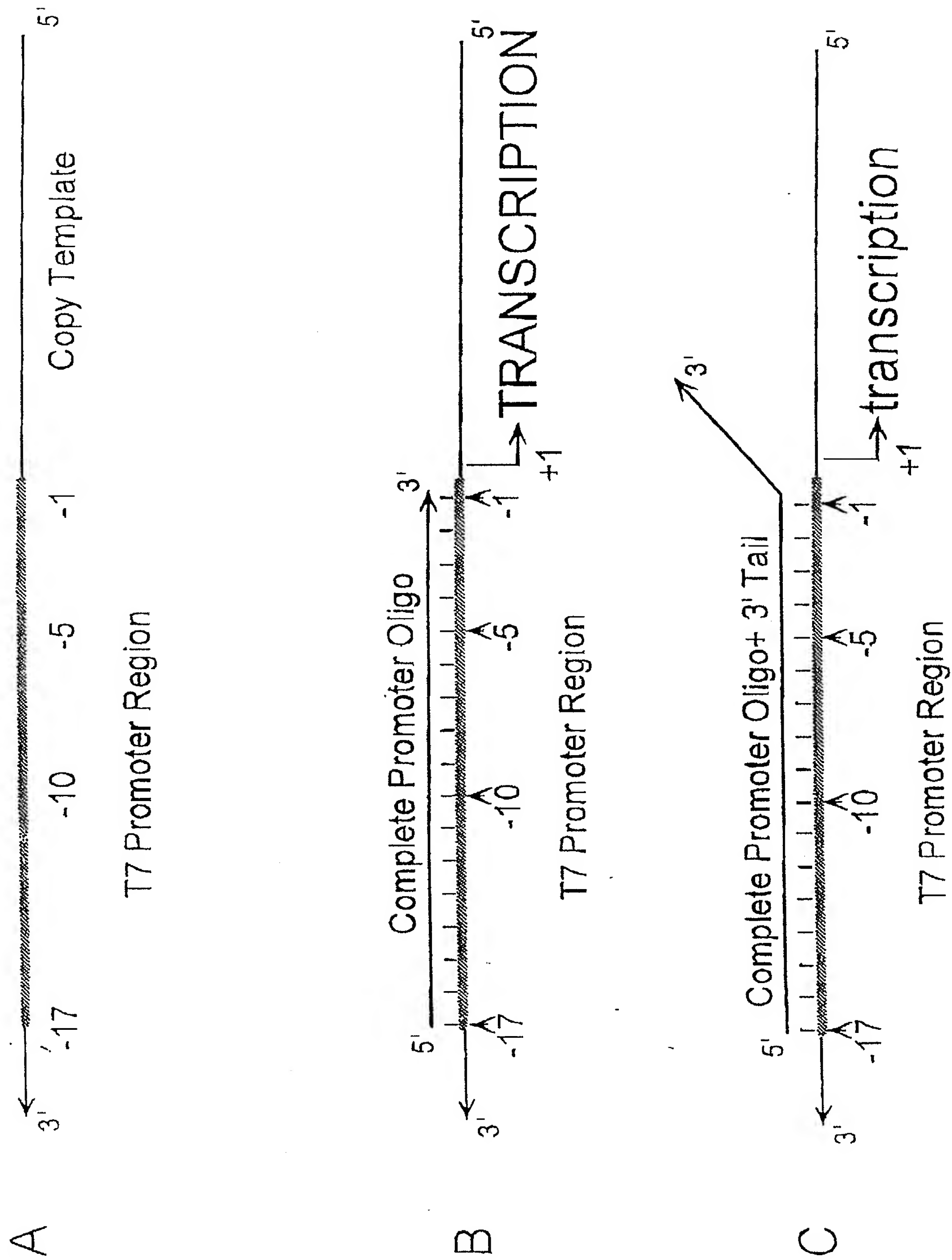


FIGURE 85



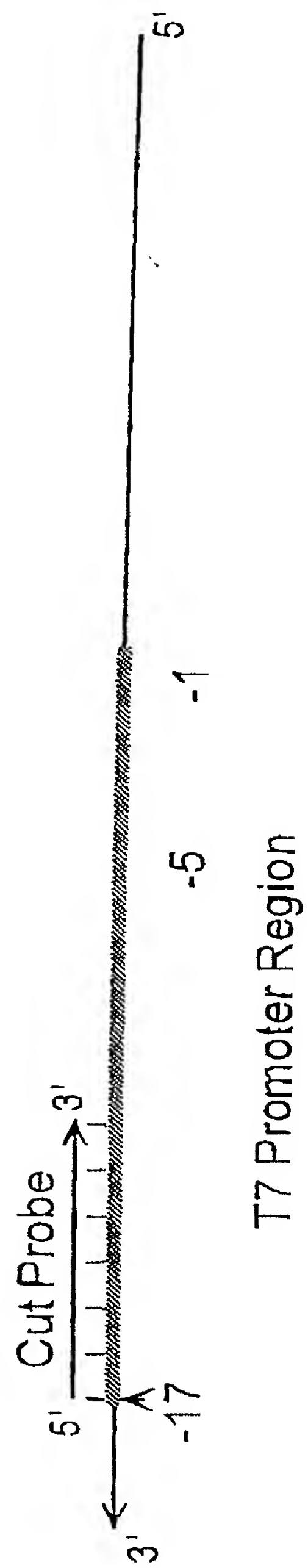


FIGURE 86A

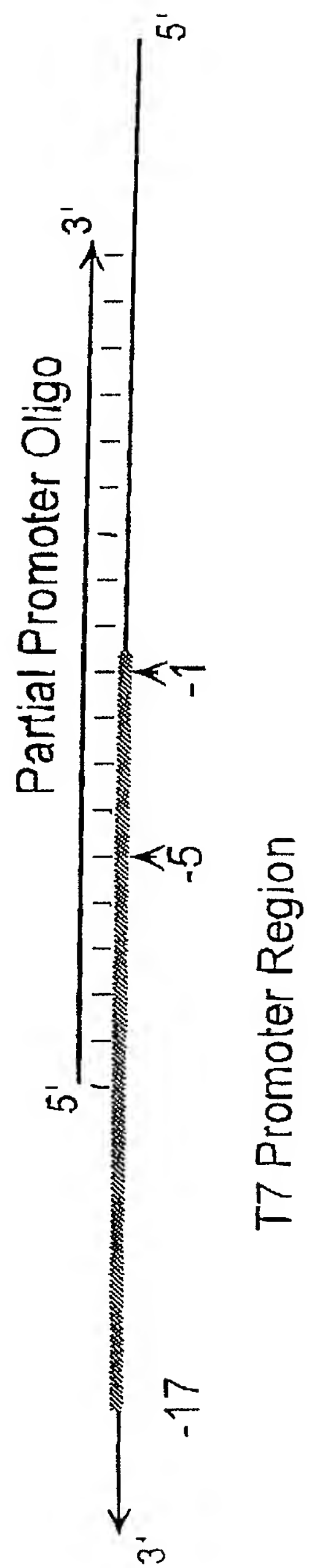


FIGURE 86B

FIGURE 86C

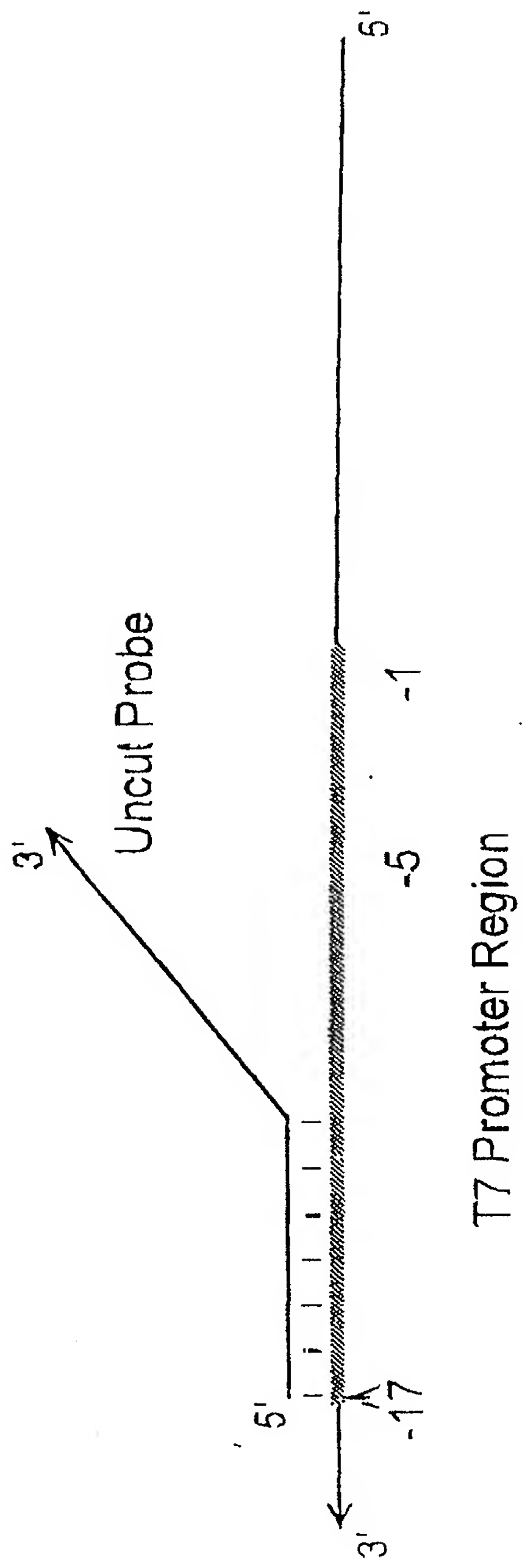


FIGURE 86D

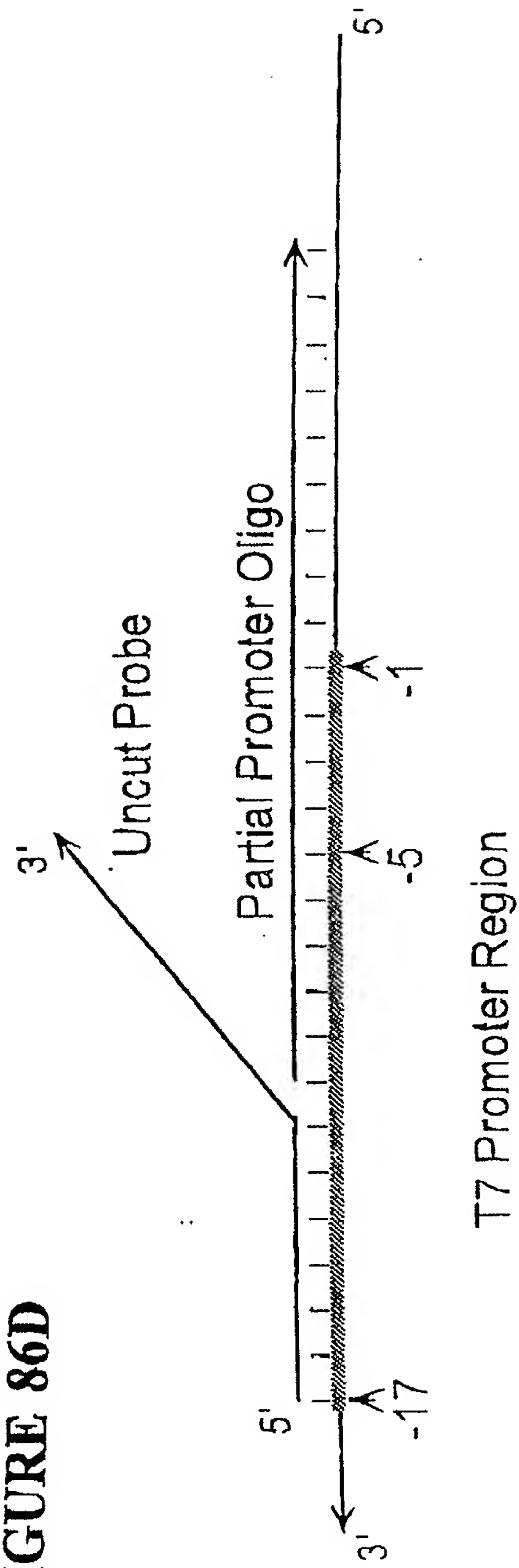


FIGURE 87

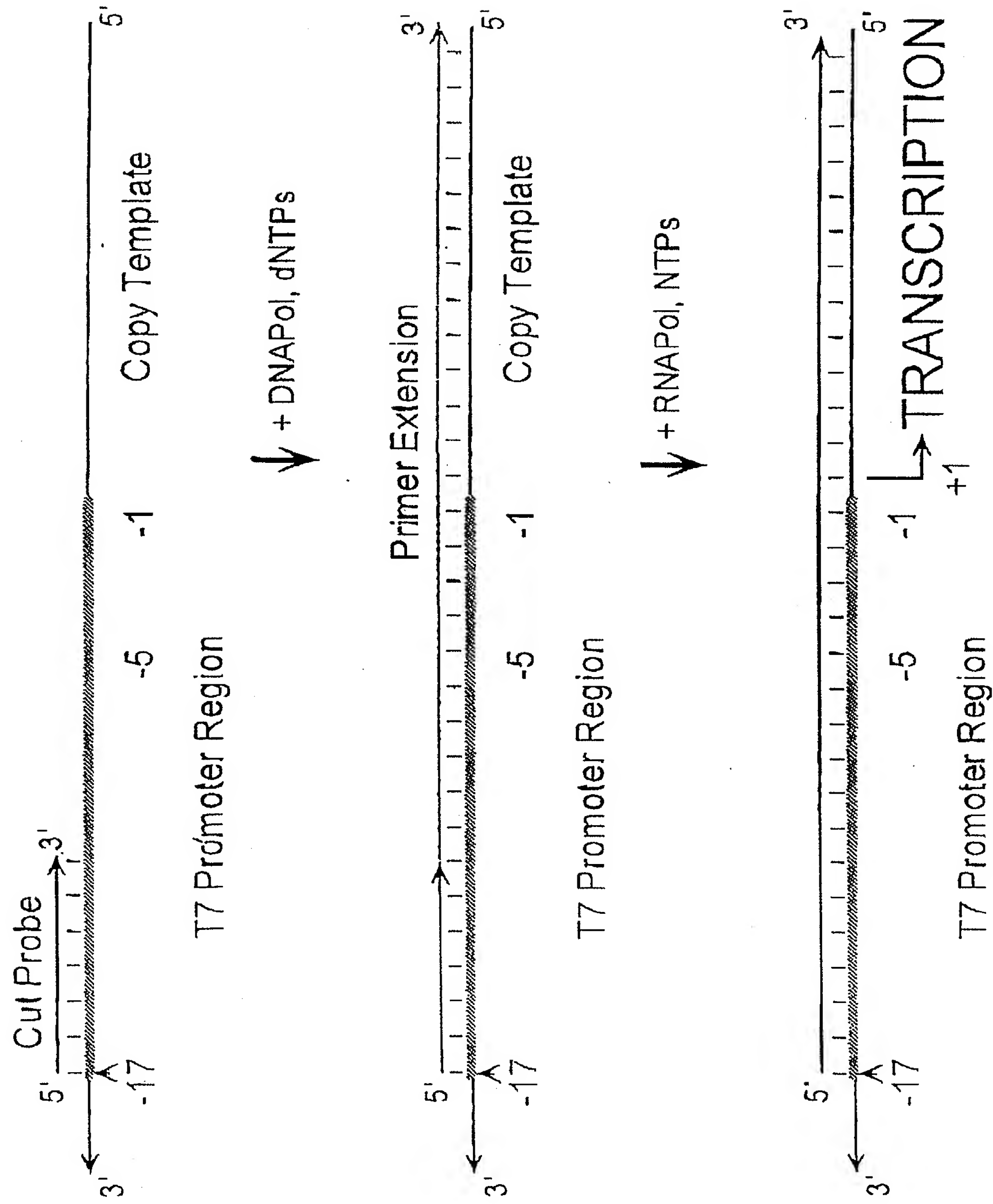


FIGURE 88A

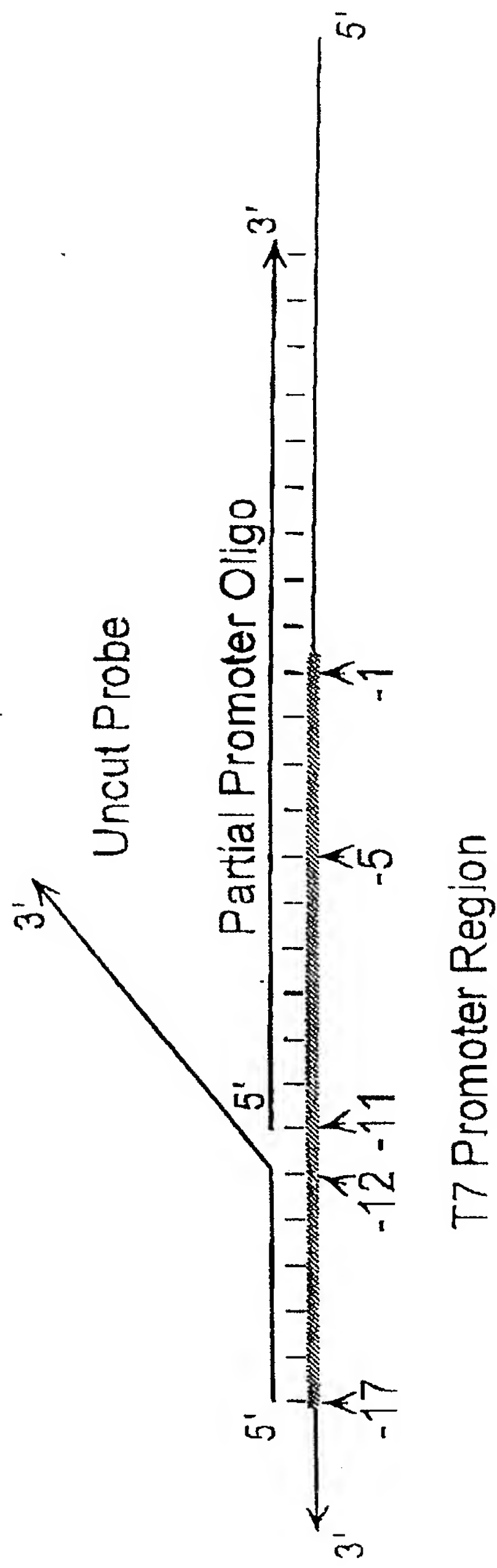


FIGURE 88B

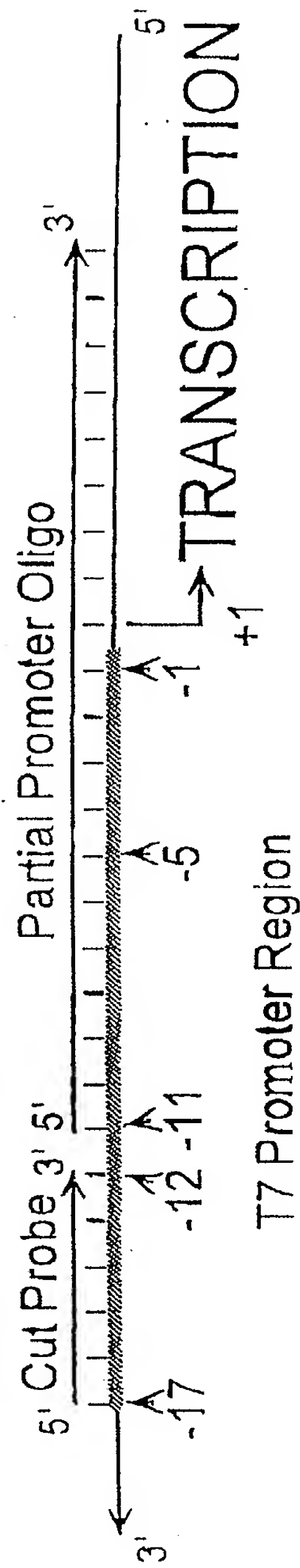


FIGURE 89

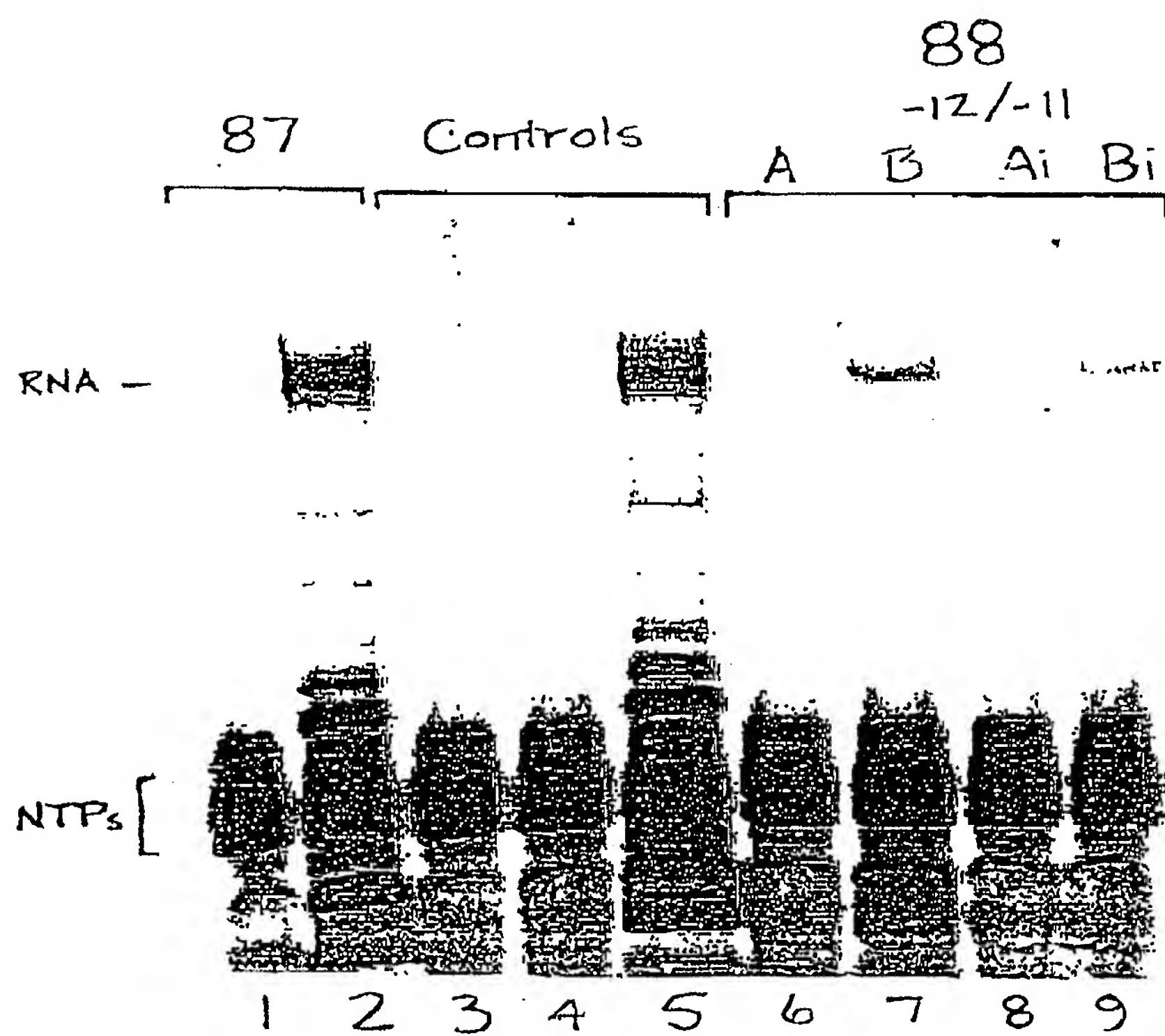
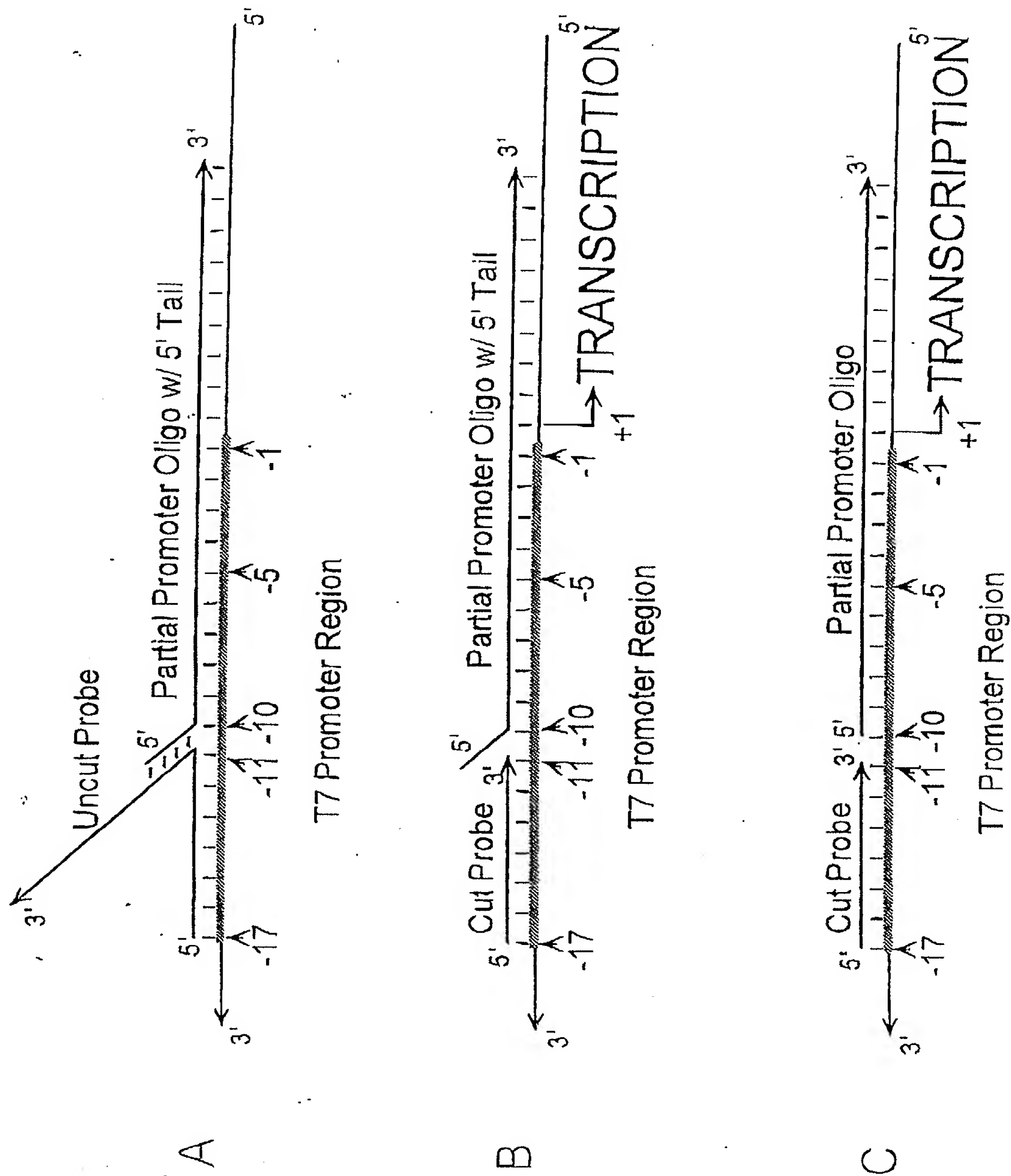


FIGURE 90



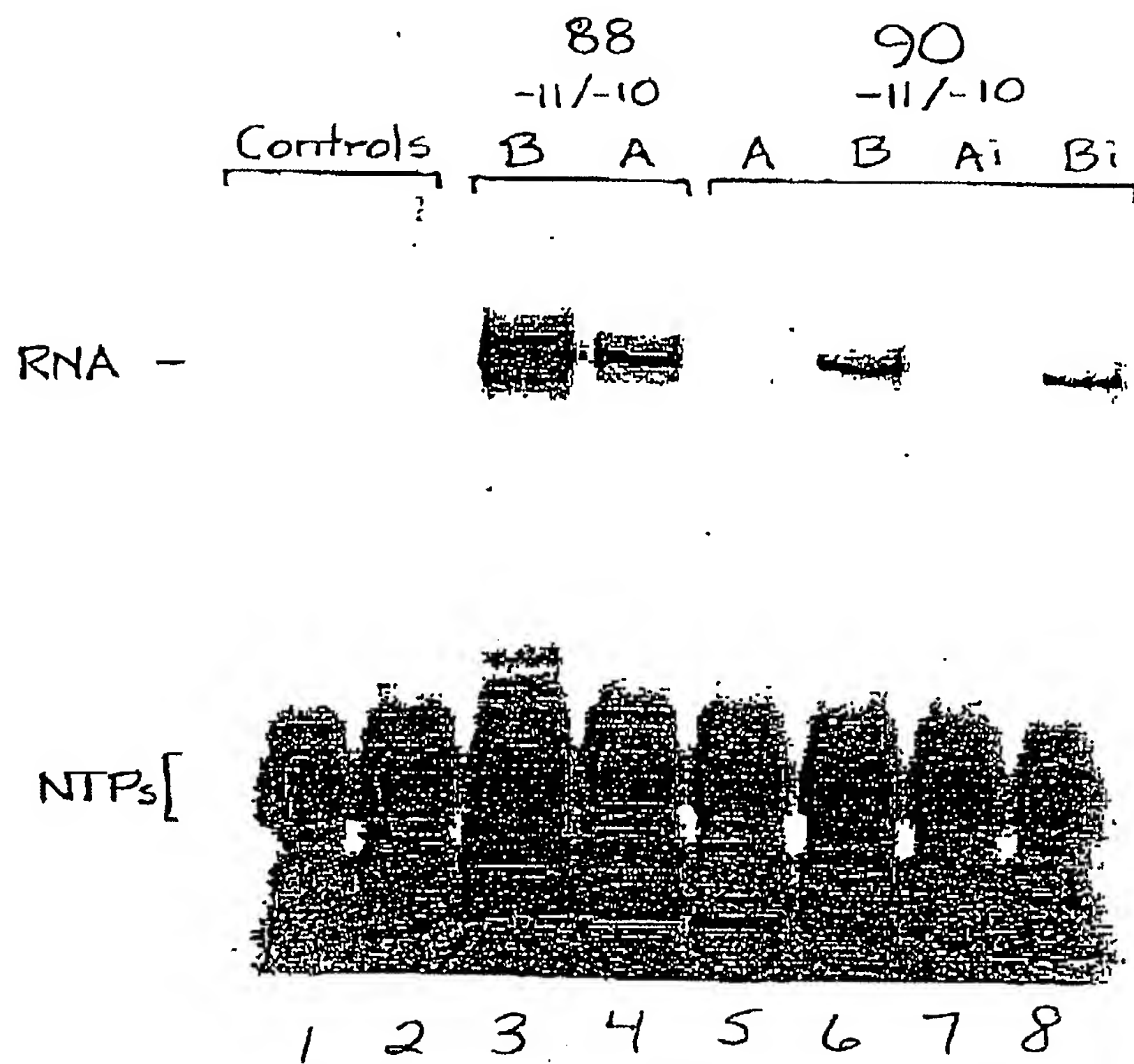


FIGURE 91

FIGURE 92

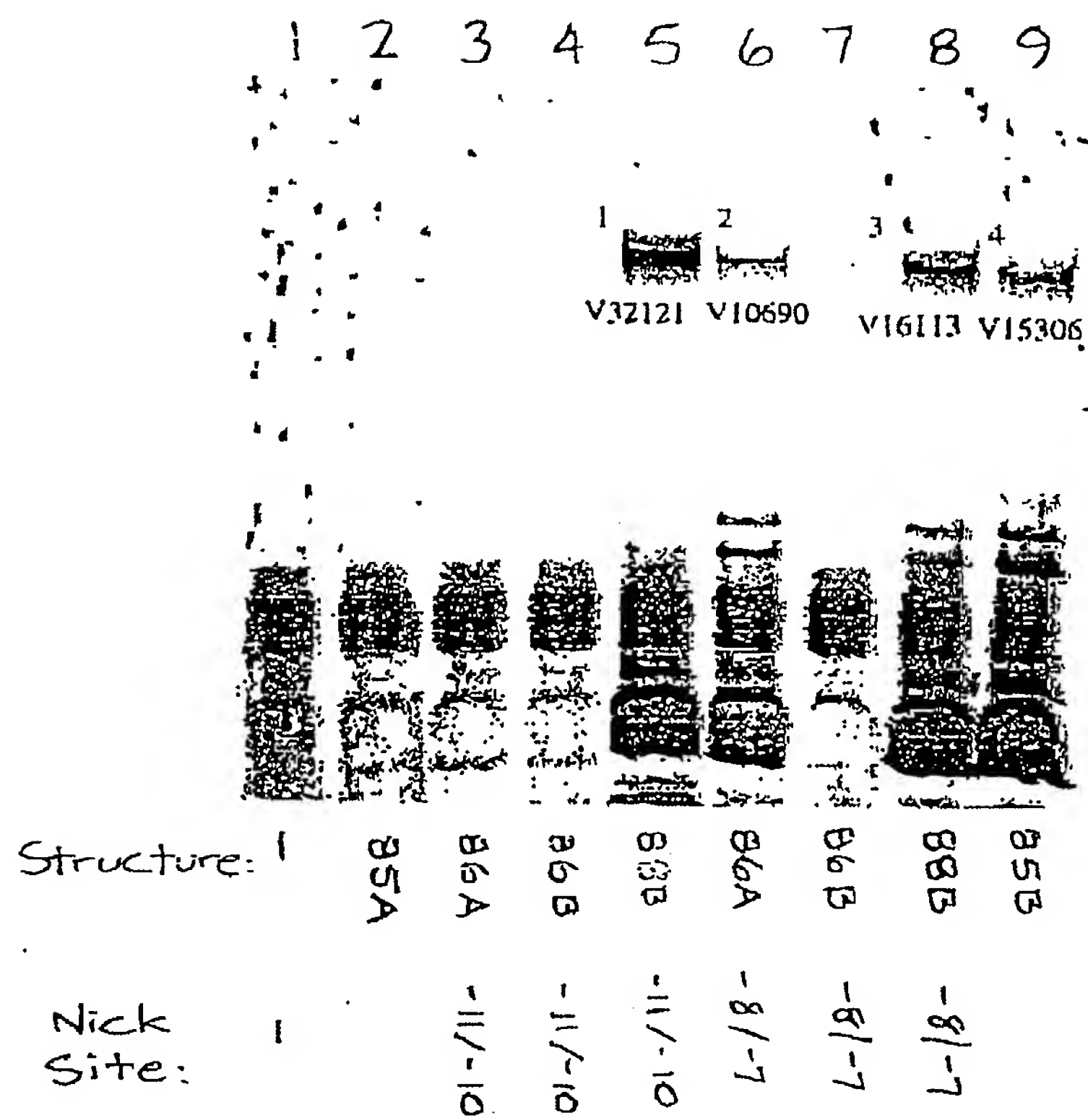


FIGURE 93

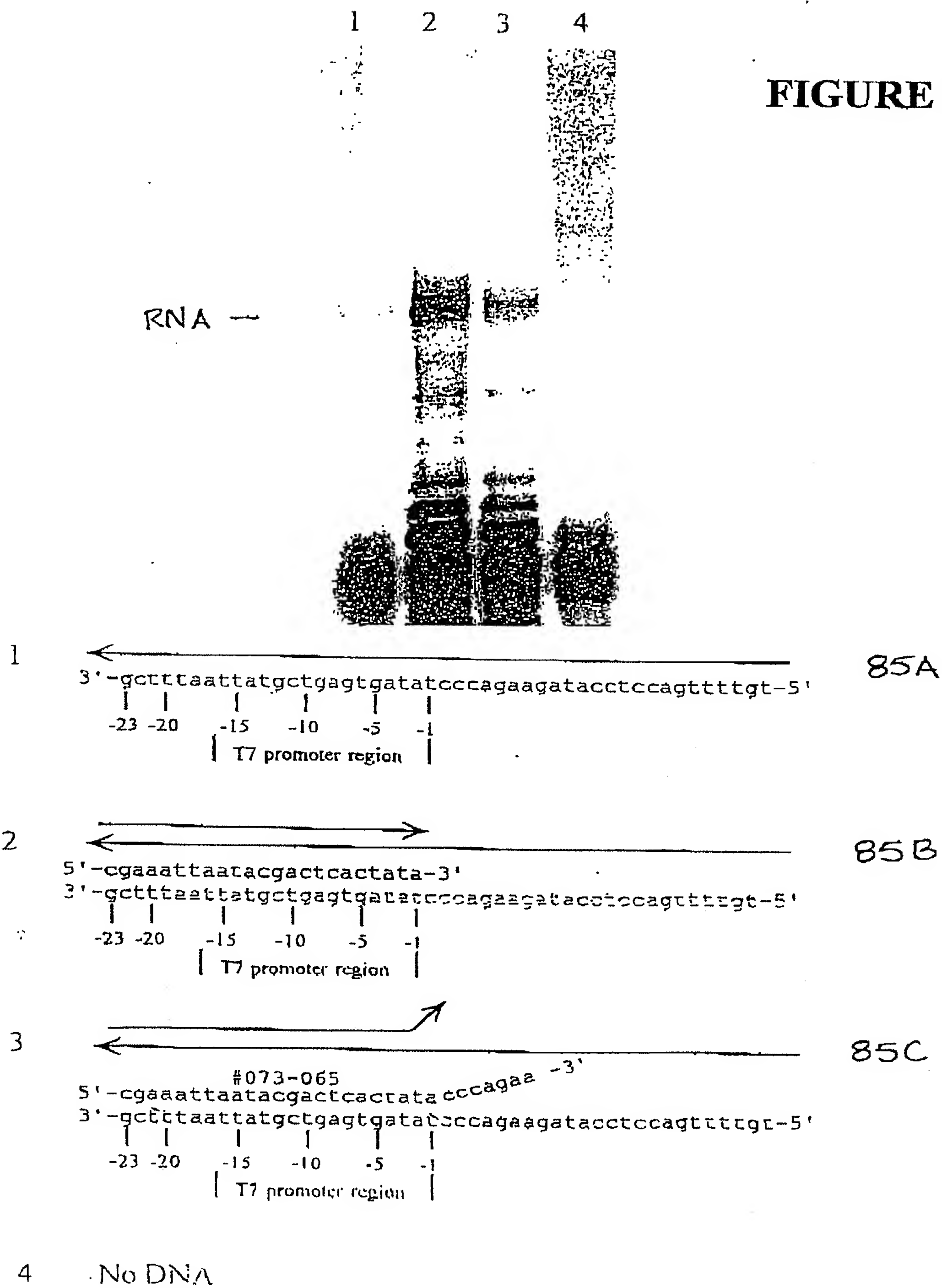


FIGURE 94

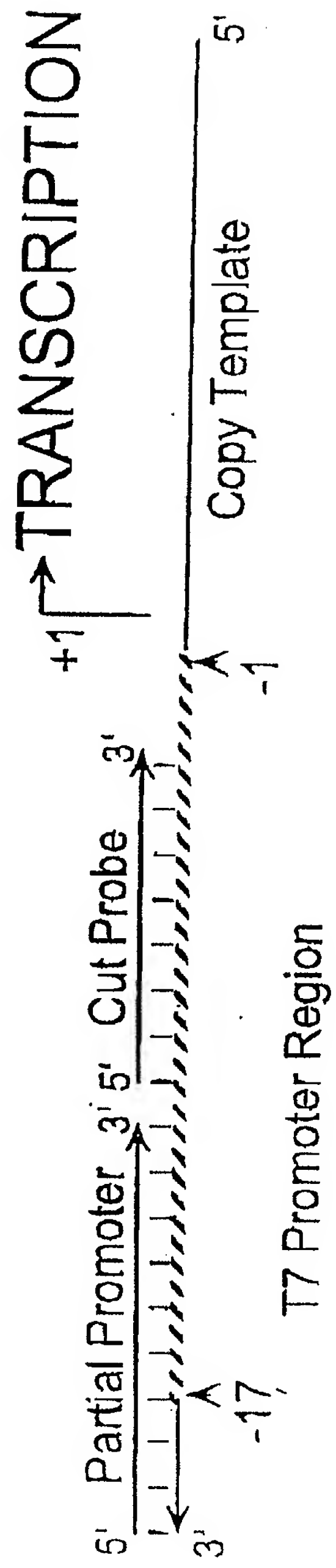


FIGURE 95A

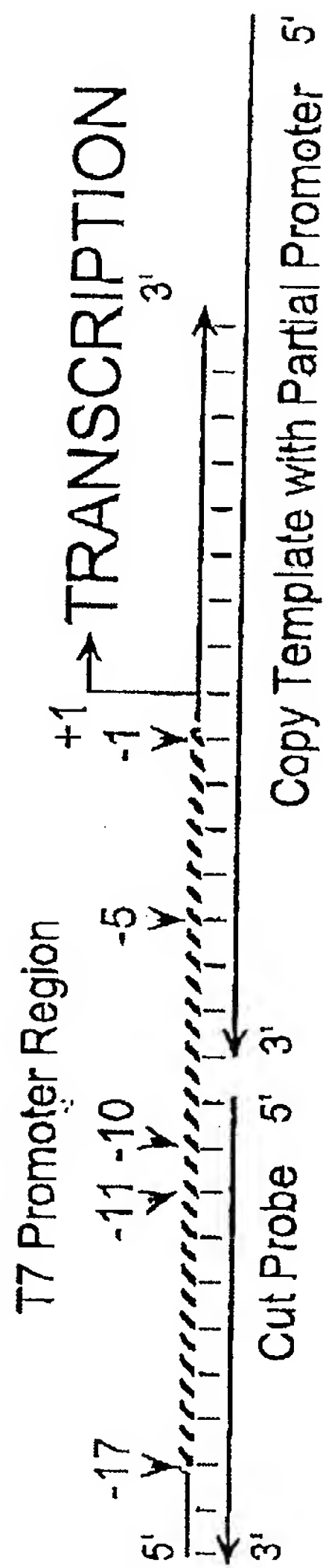


FIGURE 95B

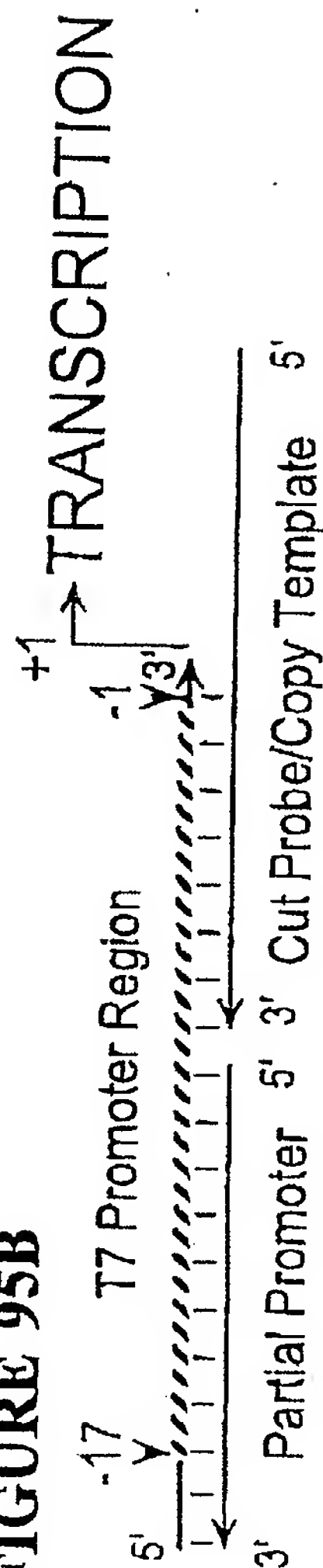


FIGURE 95C

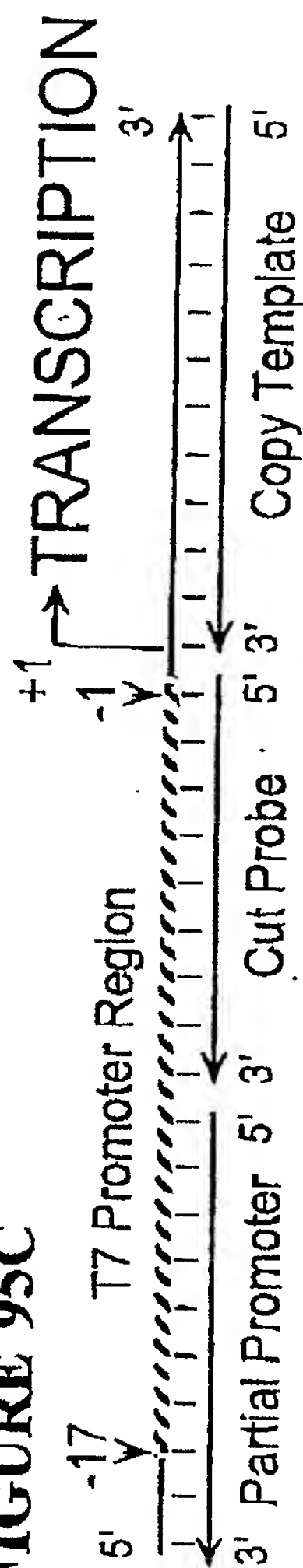


FIGURE 95D

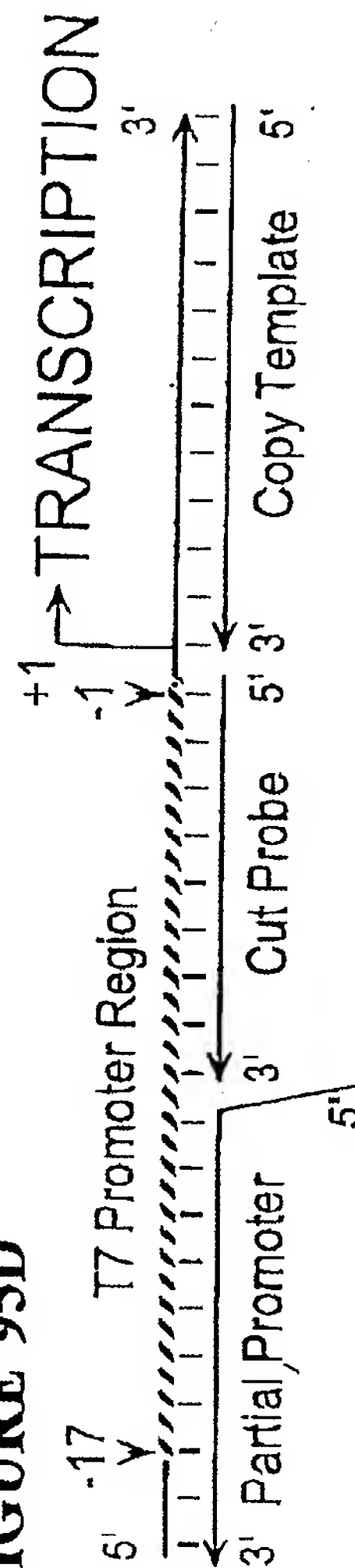


FIGURE 96

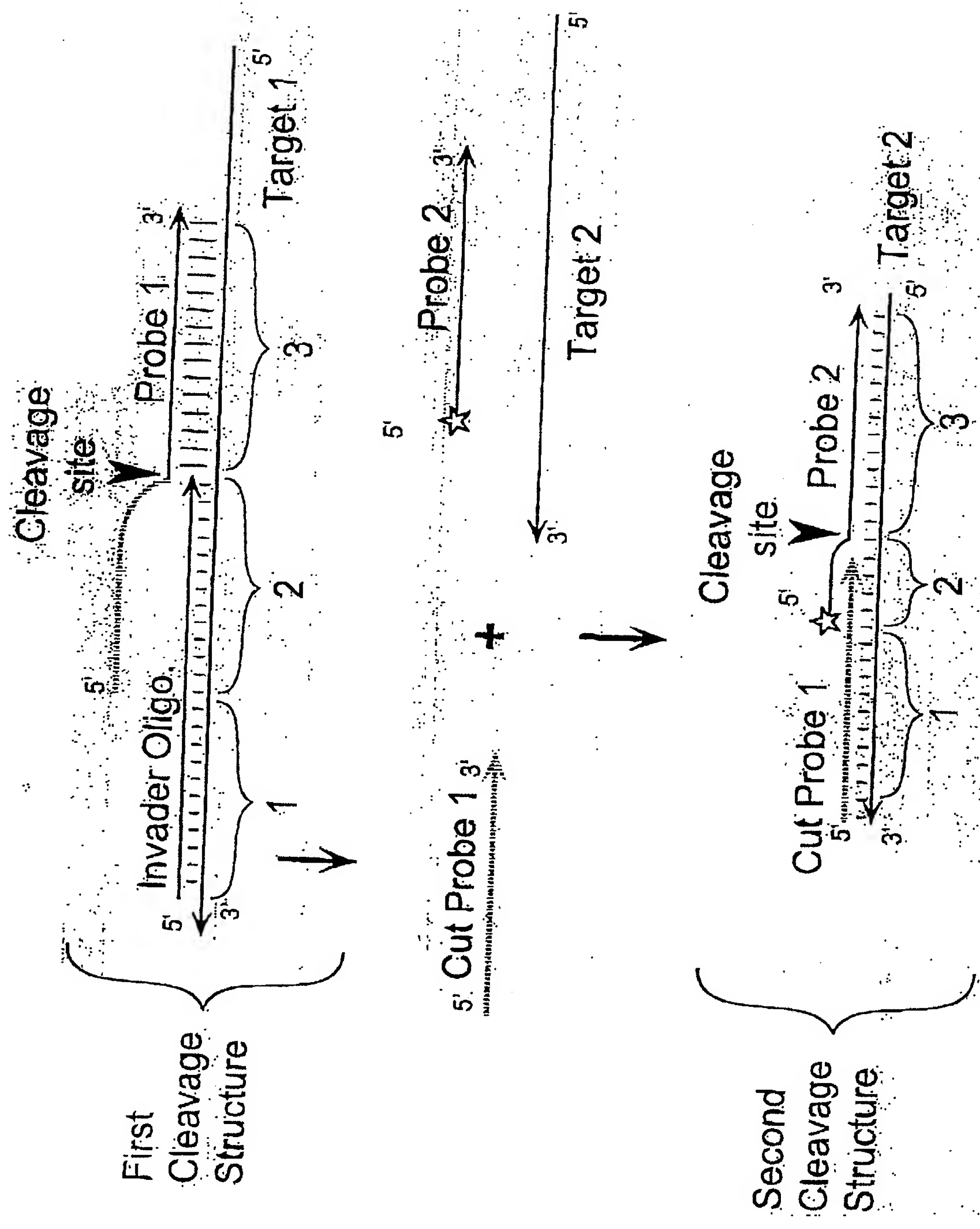


FIGURE 97

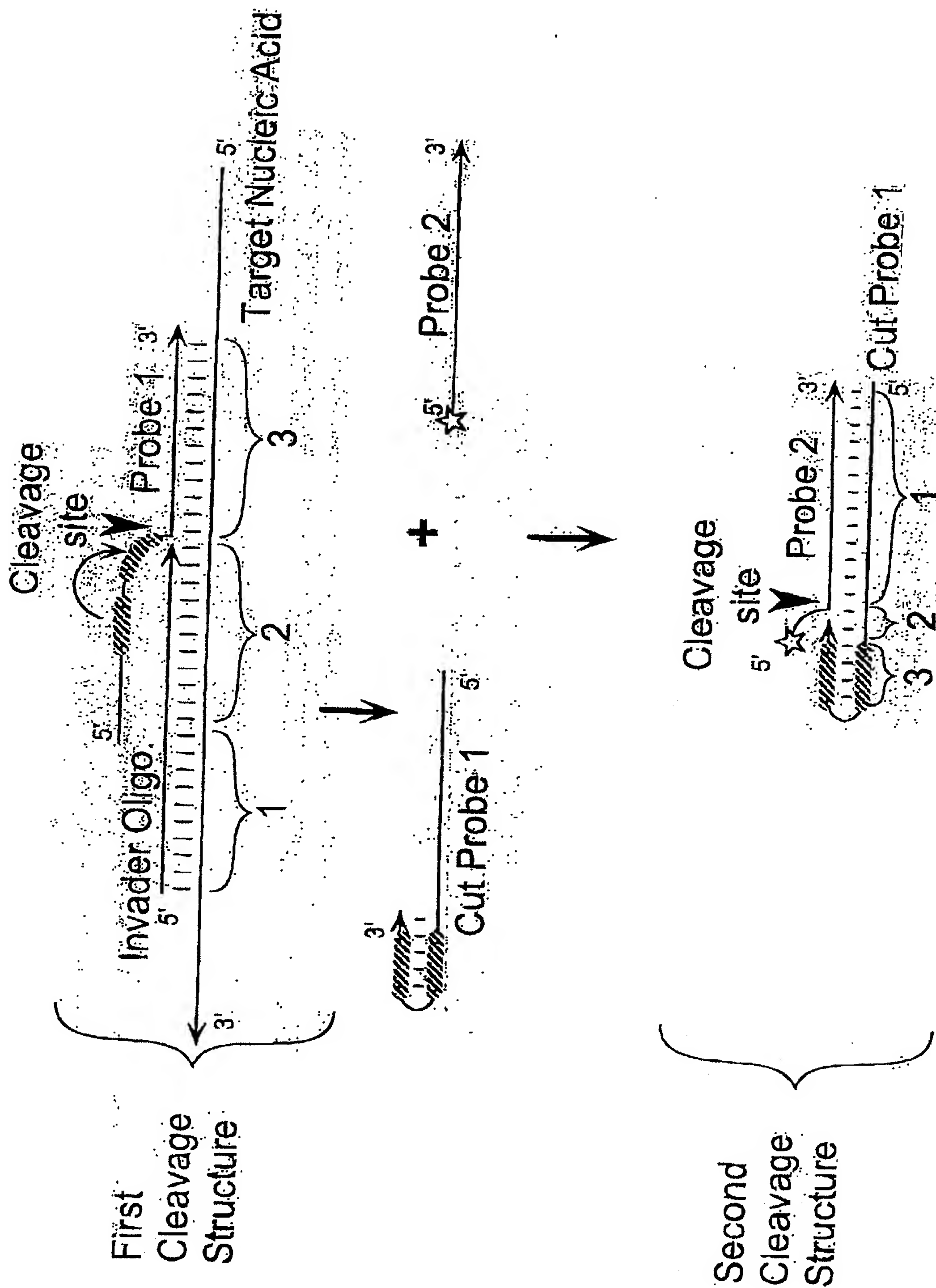


FIGURE 98

PR1 probe

Cleavage site

5'FITTTCAGAGCCTAAT G3'

IT3 Invader-Target

A^A ACGAGCGTCTTT G3'
G TGCTCGCAGAAAGGTCTCGGATTAATTTTTTTTT5'

IT3-8 Invader-Target

A^A AGCGTCTT G3'
G TCGCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-6 Invader-Target

A^A CGTCTT G3'
G GCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-4 Invader-Target

A^A TCCTT G3'
G AGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-3 Invader-Target

A^A CTT G3'
G GAAGGTCTCGGATTAATTTTTTTTT5'

IT3-0 Invader-Target

3'GAAGGTCTCGGATTAATTTTTTTTT5'

FIGURE 99

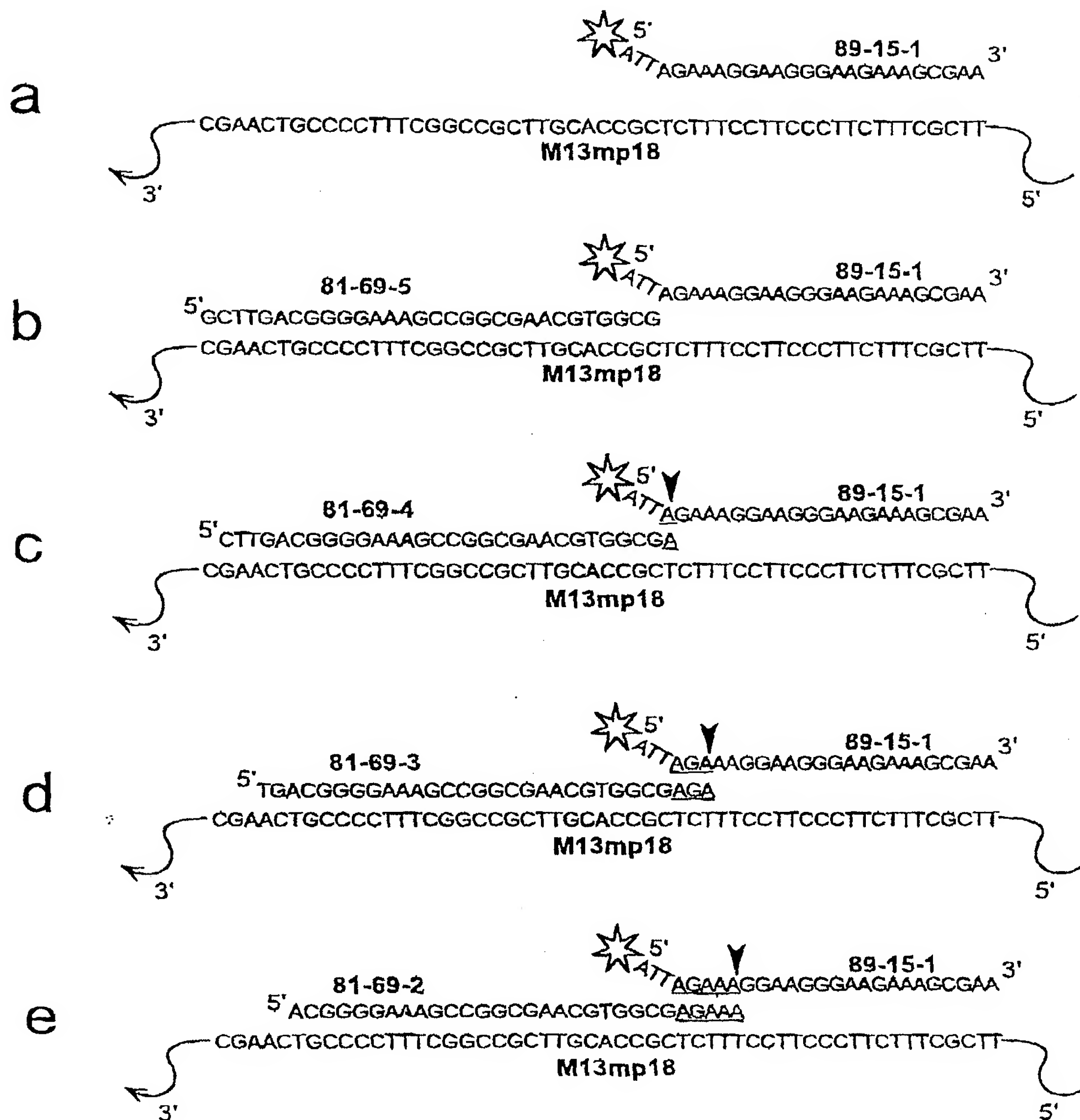


FIGURE 100

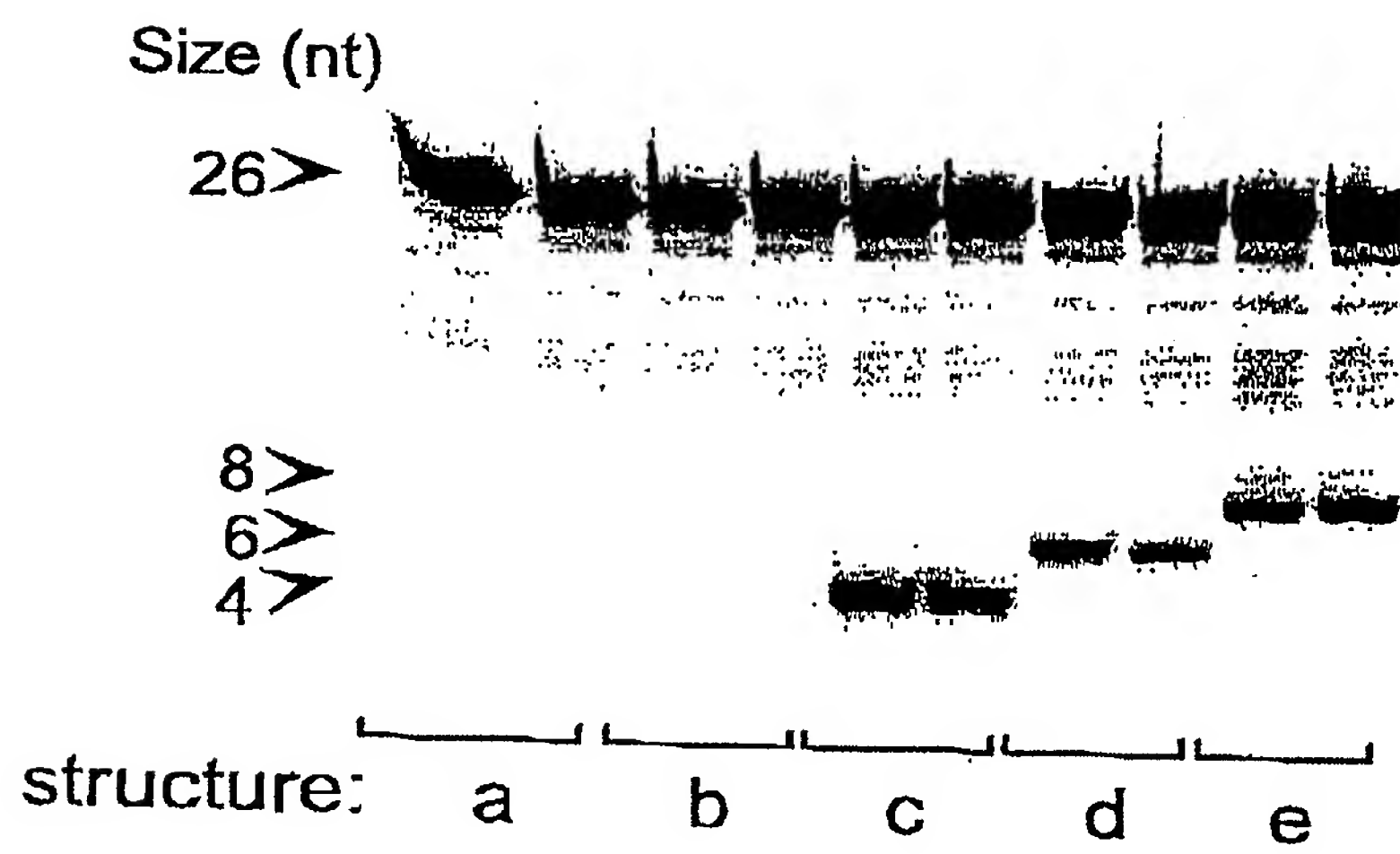


FIGURE 101

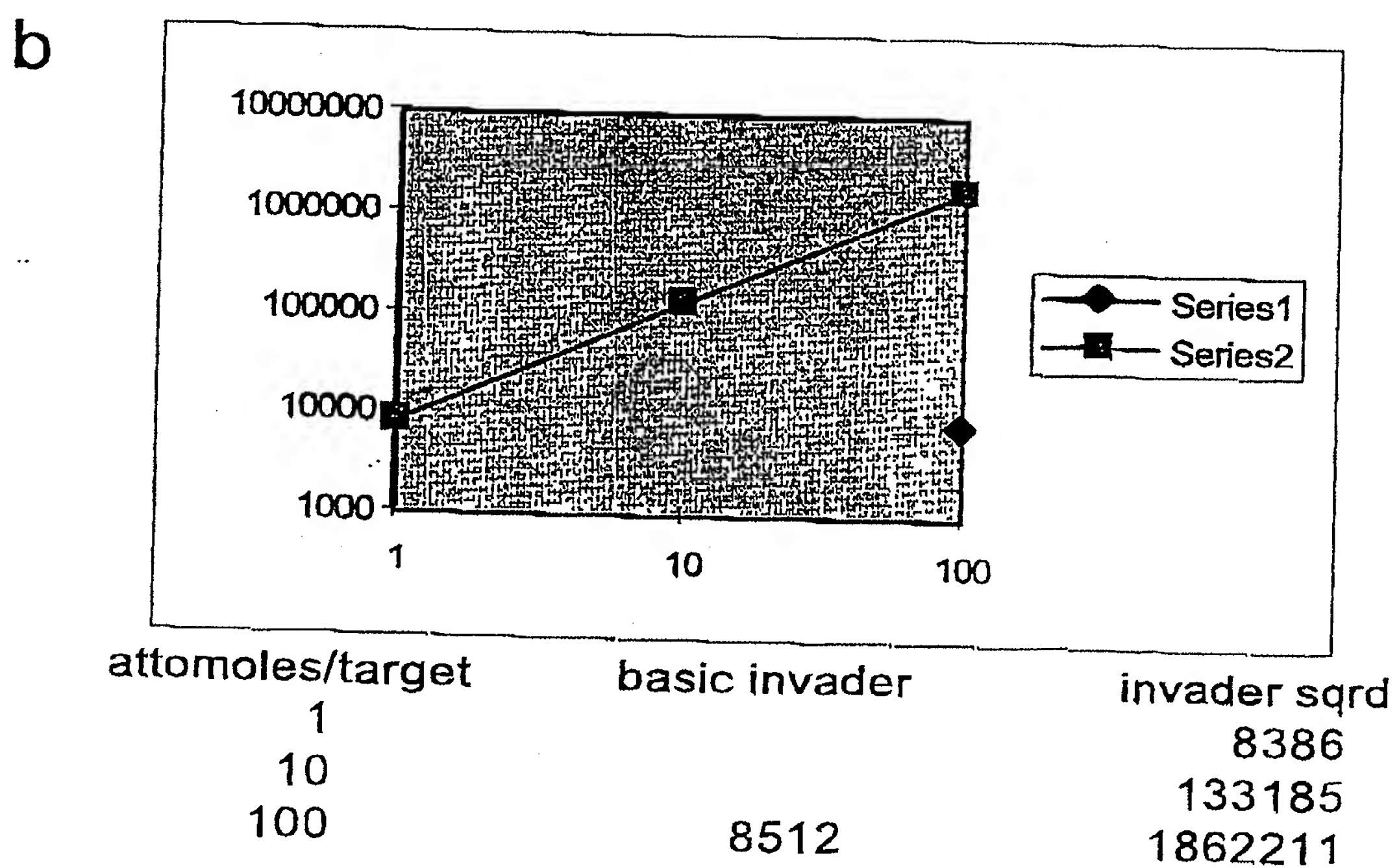
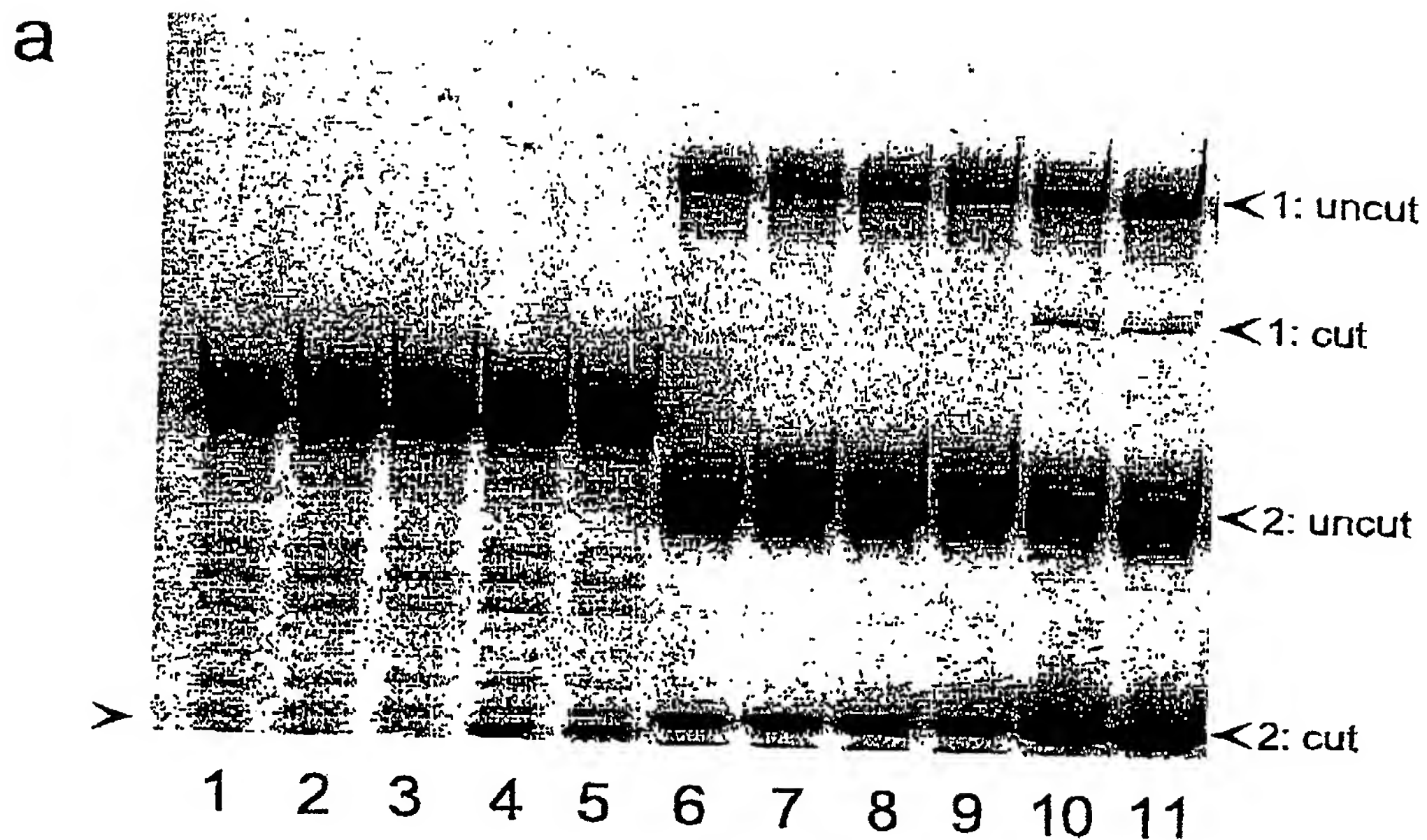


FIGURE 102

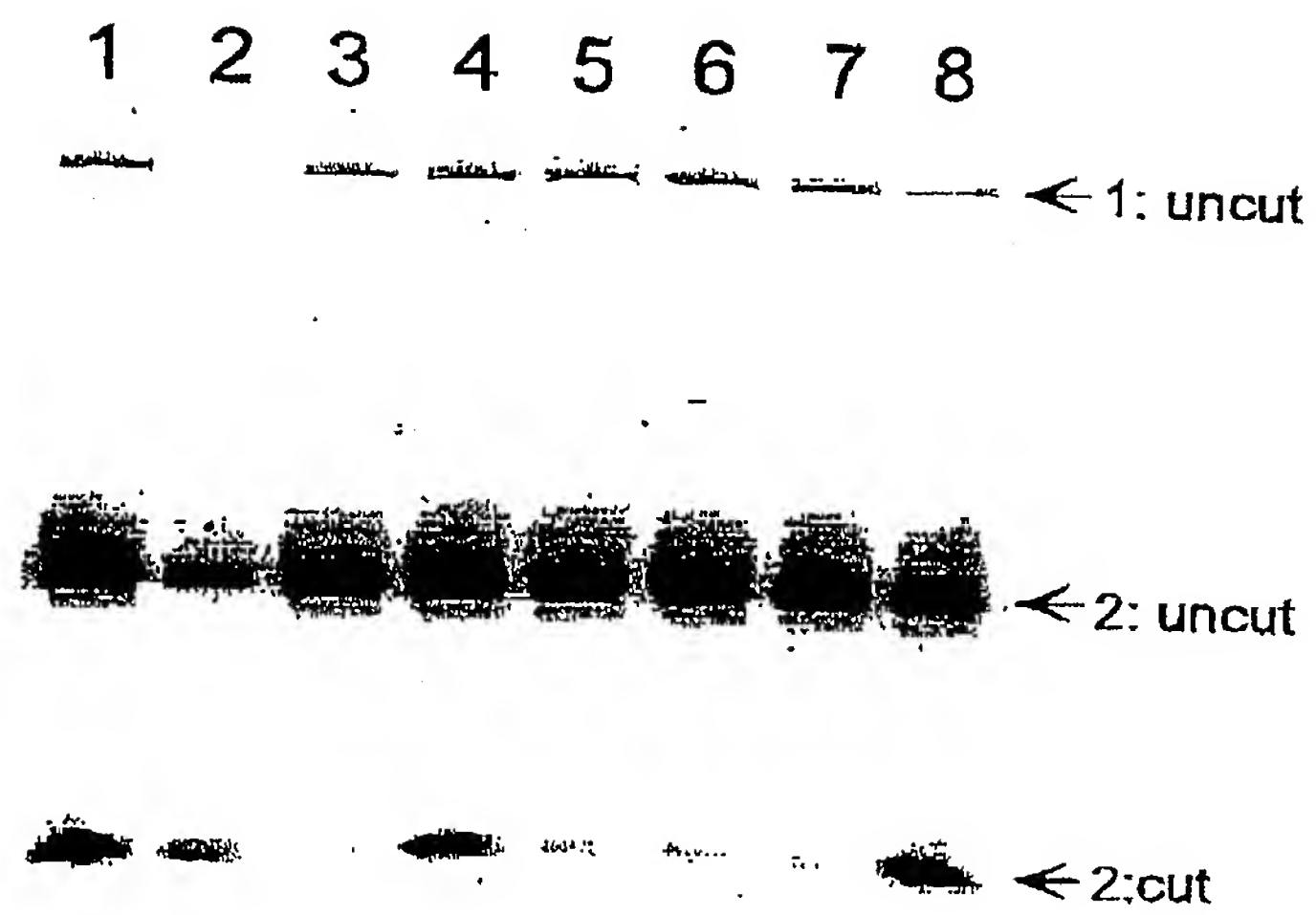


FIGURE 103

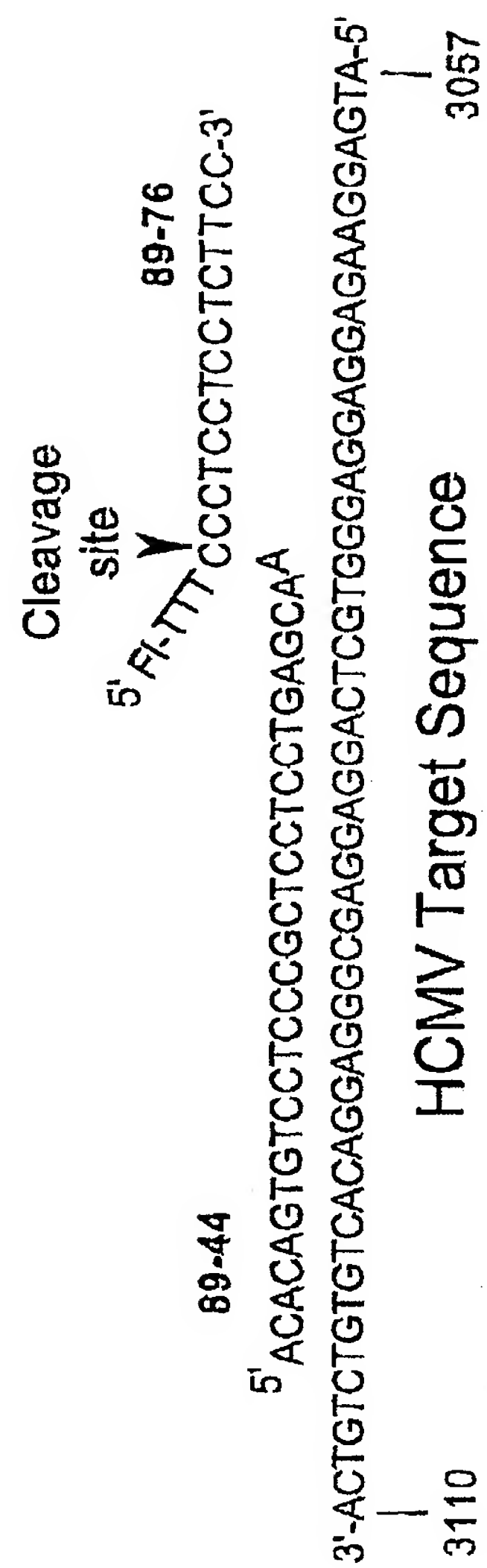


FIGURE 104

